

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 22:18:26 ; Search time 11328 Seconds  
(without alignments)

13351.596 Million cell updates/sec

Title: US-09-700-843-1

Perfect score: 11206

Sequence: 1 catgatgaataacataag.....cacgatgagaatggccagac 11206

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1047.6	9.3	1070	9	AJ281552
2	984.8	8.8	1013	10	BM438846
3	887	7.9	1004	9	AJ281480
4	874.2	7.8	935	10	BM4388279
5	839.4	7.5	841	9	AL042026
6	823	7.3	854	10	BM438950
7	742	6.6	832	10	BM438950
8	732.8	6.5	800	9	AJ281449
9	727	6.5	842	10	BM438950
10	714.2	6.4	792	10	BM438950
11	674.6	6.0	757	12	AG856202
12	669.4	6.0	754	10	BM438950
13	669.4	6.0	693	9	AL598527
14	659.2	5.9	723	12	AG107786
15	656.2	5.9	675	9	AL645322
16	654.2	5.8	717	12	AG096290
17	651.2	5.8	711	12	AG010947

c 18	649	5.8	767	9	AL040542
19	648.2	5.8	672	9	AL640799
20	647.2	5.8	671	9	AL660035
21	644.6	5.8	670	9	AL642581
22	644.2	5.7	857	12	AQ875013
23	642.6	5.7	793	12	AG000364
24	641.4	5.7	721	12	AG011001
25	638.2	5.7	702	12	AG100046
26	636.6	5.7	651	9	AL660958
27	635.2	5.7	658	9	AL656146
28	635	5.7	688	9	AL042640
29	634.6	5.7	718	12	AG105206
30	633.6	5.7	668	9	AL637190
31	633.6	5.7	850	12	AQ875052
32	631.8	5.6	798	12	AQ876139
33	631.2	5.6	695	12	AG109026
34	630.2	5.6	692	12	AG089716
35	626.2	5.6	739	12	AG095990
36	625.2	5.6	861	12	AQ875040
37	624.6	5.6	687	12	AG104968
38	624	5.6	815	12	AQ876134
39	623.4	5.6	718	9	AL631067
40	619.6	5.5	672	12	AG088034
41	619.6	5.5	699	12	AG101212
42	619.6	5.5	799	12	AQ876220
43	618.6	5.5	888	10	BI684711
44	618.4	5.5	784	12	AQ876152
45	618.2	5.5	684	12	AG112516

#### ALIGNMENTS

#### RESULT 1

AJ281552 1070 bp mRNA linear EST 30-JUN-2000  
4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles  
gambiae cDNA clone 4A3A-P6F11, mRNA sequence.

AJ281552  
AJ281552.1 GI:6929432  
EST.  
African malaria mosquito.  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
; Anopheles  
1 (bases 1 to 1070)  
Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,  
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.  
and Kafatos,F.C.  
Anopheles gambiae pilot gene discovery project: identification of  
mosquito innate immunity genes from expressed sequence tags  
generated from immune-competent cell lines  
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL  
MEDLINE  
COMMENT  
Contact: Dimopoulos G  
Fotis C. Kafatos Laboratory  
European Molecular Biology Laboratory  
Meyerhofstrasse 1, 69117 Heidelberg, Germany.  
Location/Qualifiers  
1. 1070  
/organism="Anopheles gambiae"  
/strain="4A r/r"  
/db\_xref="taxon:7165"  
/clones="4A3A-P6F11"  
/clone\_lib="Anopheles gambiae immune competent 4A3A"  
/cell\_line="E. coli DH10B"  
/lab\_host="E. coli DH10B"  
/note="vector: pT73D-Pac (pharmacia) with a modified  
polylinker; Site\_1: EcoRI; Site\_2: NotI; sequenced from  
forward priming site which reads from the 3' end of the  
cDNA. The 4A3A is a directionally cloned and normalized  
cDNA library that was constructed from the 4A3A cell line

#### FEATURES

source

oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

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BASE COUNT      263 a      283 c      255 g      269 t
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Best Local Similarity 99.5%; Pred. No. 3.3e-218;
Matches 1061; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy 8735 gagtgcggaaccccgacagagactataaagataccaggcggtttcccccctggaagctccct 8794
Db 66 gagtgcggaaccccgacagagactataaagataccaggcggtttcccccctggaagctccct 125
Qy 8795 cgtgcgtctctctgttccgacctgcggttaccgagataccctgtccgctttctcccttc 8854
Db 126 cgtgcgtctctctgttccgacctgcggttaccgagataccctgtccgctttctcccttc 185
Qy 8855 gggagcgctggcgctttctcatagctcacgctgtagtattctcagttcgggttagtgcgt 8914
Db 186 gggagcgctggcgctttctcatagctcacgctgtagtattctcagttcgggttagtgcgt 245
Qy 8915 tcgctcaagctgggctgtgtgcaagaacccccctgtccgacctgtccgctttctcccttc 8974
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Db 366 cactggtaacagagattagcagcgagggtatgtaggcgggtgctacagagttcttgaagt 425
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Db 426 gtggcctaaactcagctcacactgaagagcagattgtgtattgtctgtcgtctcgaagcc 485
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Qy 9215 cggtggtttttgtttgcaagcagcagattacgagcagaaaaaagagatctcaagaaga 9274
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Db 965 GCGCGAGCGAAGATGGCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTG 1024
Qy 9695 ccgggaagctagagtaagtagttcgccagtttaataatagtttgcgcaac 9740
Db 1025 CCGGGAAGCTAGAGTAACTAGTTGCGCAGTTAATAGTTTGGCGCAAC 1070

RESULT 2
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LOCUS      BM438846      1013 bp      mRNA      linear      EST 31-JAN-2002
DEFINITION      Iplvr00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
sequence.
ACCESSION      BM438846
VERSION      BM438846.1
KEYWORDS      GI:18460568
SOURCE      channel catfish.
ORGANISM      Ictalurus punctatus
REFERENCE      1 (bases 1 to 1013)
AUTHORS      Feng, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.
TITLE      Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
JOURNAL      Unpublished (2002)
COMMENT      Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.

FEATURES
source      1..1013
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            /db_xref="taxon:7998"
            /clone_lib="Liver cDNA library"
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            Site_2: SalI"
BASE COUNT      273 a      228 c      245 g      266 t      1 others
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Matches 1008; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

Qy 9243 attacgcgcaaaaaagatctcaagaagatcccttgatctttctacggggtctgac 9302
Db 1013 ATTACGCGCAGAAAAAAGAGATCTCAAGAGAYCCTTTGATCTTTTCTACGGGGTCTGAC 954
Qy 9303 gctcagtggaacgaacactcaogtttaaggattttggtcatgagattatcaaaaaaggatc 9362
Db 953 GCTCAGTGGAAACAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAAGGATC 894
Qy 9363 ttacacctagatcttttaataataaataaagtttaataatcaatcaatgatatagag 9422
Db 893 TTACCTAGTAGTCCTTTTAAATTAATAAATGAAGTTTAAATCAATCTAAAGTATATATGAG 834
Qy 9423 taaacttggtcagagtttaccgaatgcttaactcagtgaggccactatctcagcgatcgt 9482
Db 833 TAAACTTGGTCTGACAGTTTACCAATGCTTAATCAGTCAGGACCTATCTTCACGCGATCTGT 774
Qy 9483 ctattcgttcacccatagttgcctgactcccccgctcgtagataactacgacgagag 9542
Db 773 CTATTTCGTTCAATCCATAGTTGCTGCTGACTCCCGCTGCTAGATAACTACGATACGGGAG 714
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QY	9543	ggcttaccatctggcccccagtgctgcaatgatattacgcgagagaccacgctcaccggtctca	9602
Db	713	GGCTTACCATCTGCGCCCACTGCTGCAATGATACCGCAGACCCACGCTCACCGGCTCCA	654
QY	9603	gattttacagcaataaaacagccagccgaagggccgaagcagcagaagtggctcgtcaact	9662
Db	653	GATTTATCAGCAATAAACACAGCAGCGAAGGGCCGACGCGAGAAGTGGCTCGCAACT	594
QY	9663	ttatccgctccatccagctctattaattgttgcgggaaagctagagtagttagttcgcca	9722
Db	593	TTATCCGCGCTCCATCCAGTCTATTAAATGTGTCCGGGAAGCTAGAGTAAGTAGTTCGCCA	534
QY	9723	gtaaatagtttgcgaacgttggtccattgtctacagcatcgtggtctacgctcgtcg	9782
Db	533	GTTAATAGTTTGGCCACAGGTGTGGCAATGCTACAGGAGCATGCTGGTGTACGCTCGTGC	474
QY	9783	tttgatggtttcattcagctccggttcccaacgatcaagcgaggttaca-tgatcccc	9841
Db	473	TTTGTGTATGGCTTCATTACAGTCCGGTTCCCAACGATCAAGCGAGTTACATTGATCCCC	414
QY	9842	catgttgtgcaaaaagcgttagctcttcggtccgcatcgttggttcgaagaagtta	9901
Db	413	CATGTTGTGCAAAAAGCGGTAGCT-CTTCGGTCTCCGATCGTTGTGACAGTAAGTT	355
QY	9902	ggcgcagtggttatcactcatggttattggcagcaactgcataattcttactgtcatgcc	9961
Db	354	GGCGCAGTGTATACACTCATGTTATGGCATGACGACATGCAATTCCTTACTGTTCATGCC	295
QY	9962	atcgttaagatgctttctgtactgtagtgaactcaacaaagtcattctagaataag	10021
Db	294	ATCCGTAAAGATGCTTTTCTGTGACTGTGTGACTCAACCAAGTCNTCTGAGAATAGTG	235
QY	10022	tatgcggcagcagtggttcttctgcccgggtccaacacgggataatacogcgccacatag	10081
Db	234	TATGGCGGACGAGTGTGCTCTTGCCCGCGTCAATACGGGATATATACCGGCCACATAG	175
QY	10082	cagaactttaaagtgctcatcttgataaaacgttcttcggggcgaaaactcgaagat	10141
Db	174	CAGAACTTTAAAGTGCTCATCATTTGGAAACGTTCTTCGGGGCGAAACTCTCAAGAT	115
QY	10142	cttaacgctgttgatgataccagttcgatgtaacccaactcgtgcaccaacgtatctcagc	10201
Db	114	CTTACCGCTGTGTAGATCCAGTTTCGATGTAAACCACTCGTGCACCAACTGATCTTCAGC	55
QY	10202	atcttttacttccacagcgttctcgttgtagcaaaaacaggaagcaaaatgc	10255
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DEFINITION	4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P4G8, mRNA sequence.		
ACCESSION	AJ281480		
VERSION	AJ281480.1	GI:6929360	
KEYWORDS	EST.		
SOURCE	African malaria mosquito.		
ORGANISM	Anopheles gambiae		
REFERENCE	1 (bases 1 to 1004)		
AUTHORS	Dimopoulos, G., Casavant, T. L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultze, J., Benes, V., Borik, P., Ansoorge, W., Soares, W. B. and Kafatos, F. C.		
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (12), 6619-6624	(2000)
MEDLINE	20300950		
COMMENT	Contact: Dimopoulos G		
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	/lab_host="E. coli DH10B"		
	/note="Vector: pT7R3D-Pac (Pharmacia) with a modified polylinker; Site.1: EcoRI; Site.2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."		
BASE COUNT	252 a 262 c 244 g 244 t		
ORIGIN			
Query Match	7.9%; Score 887; DB 9; Length 1004;		
Best Local Similarity	98.0%; Pred. No. 4.5e-183;		
Matches 970; Conservative	1; Mismatches 12; Indels 7; Gaps 7;		
QY	8662	atttcaagaagaagcgtttttccataggtccgcgcctccctcgcagcagcatcacaaaatc	8721
Db	22	AGGCGCGTGTGCTGGCGTTCATAGGCTCCGCCCTCGACGAGCATCAAAAATC	81
QY	8722	gacgtcaagtcagaggtgcgaaacccagcagactataaagataccaggcgttcccc	8781
Db	82	GACGCTCAAGTCAGAGGTGGCGAAACCGACAGACTATAAAGATACAGCGGCTTCCCC	141
QY	8782	ctggaggtccctcgtgcgtctctcgttccgaccctgcgccttacccgataactgtcgc	8841
Db	142	CTGGAAGCTCCCTCGTGGCGTCTCTGTTCCGAGCCTTACGGATACCTGTCCG	201
QY	8842	ctttctcccttcggaaagcgtggcgtttctcaatcactcacgttagtattctcagtt	8901
Db	202	CTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTT	261
QY	8902	cggtgtagctctgcgtccaaagctggcgtgtgscgaaccccccgcttcagccgcac	8961
Db	262	CGGTGTAGGTCTGCTCCAGCTGGGCTCTNTGTCAGAACCCCGCTTCAGCCGAC	321
QY	8962	gctgcgcttaccggttaactatcgtttgagtcacaaccccggttaagacagcactatcgc	9021
Db	322	GCTGCGCTTATCCGGTAACATATGCTTTGAGTCCAAACCCGGTAAGACACGACTTATCG	381
QY	9022	cactgcagcagccactggttaacaggttagcagcgaggtatgtaggcggtgctacag	9081
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QY	9142	ctctgtgaagcaggttaccttcgaaaaaagttggtagctcttgcgcgcgcaacaa	9201
Db	502	CTCTGTGAAGCAGTTACTTCGGAAAAAGAGTTGGTAGTCTTTGATCCGGCAACAA	561
QY	9202	ccacgcgtgtagcgggtgttt	9261
Db	562	CCACCGCTGTTAGCGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	621
QY	9262	gatctcaagaagatccttttgatcttttttctacggggtctgacgctcagtggaagaaact	9321
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Db 682 CACGTTAAGGATTTGGCTGATGAGATTATCAAAAAGGATCTTCACCTAGATGCTTTTAA 741  
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Db 919 GTGCTGCAATATACCGGAGA-CCAGCHCA-CGCTCCAGATTT-TCAGCAATAAACC 975  
QY 9622 agccagccggaaggccgagcaggaagt 9651  
Db 976 AGCCAGCCGGAA-GGCCGAGCGCAGAAGTG 1004

RESULT 4  
LOCUS BG838279/c 935 bp mRNA linear EST 25-MAY-2001  
DEFINITION Gc01\_10e07\_R Gc01\_AAFc\_ECORC\_cold\_stressed\_Glycine\_clandestina  
Glycine clandestina cDNA clone Gc01\_10e07, mRNA sequence.

ACCESSION BG838279  
VERSION BG838279.1 GI:14204601  
KEYWORDS EST.  
SOURCE Glycine clandestina.  
ORGANISM Glycine clandestina.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

1 (bases 1 to 935)  
Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris  
,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker  
,N.A.

Expressed Sequence Tags from Cold-Stressed Glycine clandestina  
Seedlings  
Unpublished (2001)  
Contact: Singh,J.A.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA 0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@em.agr.ca

Location/Qualifiers  
1..935  
/organism="Glycine clandestina"  
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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI;  
Site\_2: XhoI; Plants incubated at 2 degrees under 12 hours  
of light/dark. Harvested after only 2-3 days of cold  
treatment. cDNA was prepared with the Uni-Zap cDNA kit  
from Stratagene. Eco RI adapters were linked followed by  
digest with Xho I/Eco RI and ligated to pBluescript."

BASE COUNT 243 a 213 c 227 g 238 t 14 others  
ORIGIN

Query Match 7.8%; Score 874.2; DB 10; Length 935;  
Best local Similarity 97.6%; Pred. No. 2.8e-180;

Matches 881; Conservative 14; Mismatches 7; Indels 1; Gaps 1;  
QY 9539 ggagggttaacatctgccccagtgctgcaatgatacccgagagaccacgctcacggc 9598  
Db 928 GGGGGGCTTACCATCTGCCCCAGKGTGCAATGATACCGGAGMCCACGCTCMCCGGC 869  
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Db 868 YCCAGATTTATCAGCAATAAMCCASCAGCCGGAAGGGCGGAGCAGAAAGTGGTCTGC 809  
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Db 808 AMCTTTATCCGCCCTCCATCCAGTCTATTAAATTGTCGGGAAGCTAGAGTAAGTAGTTC 749  
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JOURNAL Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
COMMENT EST (Poustka, et al.)
Unpublished (1999)
Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp434E111) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Poustka, et al.)  
Unpublished (1999)  
Contact: Poustka A.J.  
Department Lehrach  
Max-Planck-Institute for Molecular Genetics  
Ihnestrasse 73, 14195 Berlin, Germany  
Tel: +49-30-84131623  
Fax: +49-30-84131128  
Email: poustka@mpg-berlin-dahlem.mpg.de  
This is the 5' sequence of the clone insert  
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Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
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No si sequence available.  
This clone (DKFZp434E111) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabps-femail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM10915 row: j column: 23 High quality sequence start: 32 High quality sequence stop: 823.			
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AUTHORS Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultze, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.			
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JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc.			

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 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
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<http://image.llnl.gov>

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 Best Local Similarity 96.3%; Pred. No. 4.4e-145;  
 Matches 798; Conservative 0; Mismatches 25; Indels 6; Gaps 5;

Qy 9585 ccagctccacggctccagatttatcagcaataaacacagcagcggaagggcgagcgc 9644  
 Db 7 CCAGCTCACCGGCTCCAGATTATCAGCAATAAACCCAGCCGAGGCGCGAGCGC 66  
 Qy 9645 agaagtggtcctgcaactttatccgctccatccagctcatttaattgttgcgggaagct 9704  
 Db 67 AGAAGTGGTCTCGCACTTTATCCGGCTCCATCCAGTCTATTAAATGTTGTCGGGGAAGCT 126  
 Qy 9705 agagtaagtagtgcgcagtaagattgtgcgaacggtgttgccattgctacagga-t 9763  
 Db 127 AGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCAAGGTTGTCATCGCTACAGGCCT 186  
 Qy 9764 cgtggtcacgctcgtcgt-ttggtatggttcattccatccagctccggttcccaacgataca 9822  
 Db 187 CGTGGTCTACGCCCTCCCTCTGGTATGGCTTCATTCAGCTCCGCTTCCCAACAGATCAA 246  
 Qy 9823 ggcaggtacatgatcccccatgttgcaaaaagcggttagctccttcggtctccga 9882  
 Db 247 GCGAGTTACATGATCCCCCATGTTGTGCAAAAAGCGTTAGCTCTCGTCTCCGA 306  
 Qy 9883 tcgtgtcagaagtaagttggcgcagtggttatcactcgtggtatggtgcagcaactgcata 9942  
 Db 307 TCGTGTGTCAGAAGTAGTTGGCGCAGTGTATCACTCATGTTTATGGCAGCACTGCATA 366  
 Qy 9943 attctctactgcatgccatccgtaagatgctttctgtgactggtgactactcaacca 10002  
 Db 367 ATTCCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGCTGAGTACTCAACA 426  
 Qy 10003 agtcattctgagaaatagtgatgagcgacccaggtgtccttggccggcggtcaaacggg 10062  
 Db 427 AGTCATTCTGAGAATAGTGTATCGCGGACCGAGTTGCTCTTTGCCGCGCTCAATACGGG 486  
 Qy 10063 ataataccgcgcacatagcagaactttaaaagtctcattgtaaaaagttcttcgg 10122  
 Db 487 ATATACCGCGCCACATAGCAGAACCTTAAAGTGCTCATCATTTGAAACACGTTCTTCGG 546  
 Qy 10123 ggcgaacactcgaagatcttaccgctgttgagatccaggttcgatgtaa-ccceactcgt 10181  
 Db 547 GCGCAAAACTCTCAAGATCTTACCCTGTTGAGATCCAGTTCGATGAACCCCACTCGT 606  
 Qy 10182 gcaccaactgacttcagcatcttttacttttaccagaggtttctcgggtgagcaaaaaa 10241  
 Db 61 AATTGTTGCCGGGAAGCTAGTAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTT 120

Db 607 GCACCCAACTGATCTTTCAGCATCTTTTACTTTCACCAAGCTTTCTGGTGAGCAAAAAACA 666  
 Qy 10242 ggaagcaaaaatgcccgaaaa-aaggaataagggcgacagcgaataatgtgaatactcat 10300  
 Db 667 GGAAGCAAAATGCCCAAAACAAGGAATAAGGGCGACACAGGAATGTTGAATACTCAT 726  
 Qy 10301 actctccctttttcaat--attattgaagcatttatcaggggttattgtctcatgagcgga 10358  
 Db 727 ACTCTCCCTTTTCAATCACTCATCGAAGCATCTATCAGGGTTATCGTCTCATGAGCGGA 786  
 Qy 10359 tacatttggaatgtatttagaaaaataaacaataaggggttcccgcca 10407  
 Db 787 TACTACTGTCATGTATTAGGCAAAATTAACAATAGGGGTCCGCGCCCA 835  
 RESULT 10  
 Bi687057  
 LOCUS 603312478F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5352714 5',  
 DEFINITION mRNA sequence.  
 ACCESSION Bi687057  
 VERSION Bi687057.1 GI:15649685  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM1896 row: k column: 19  
 High quality sequence stop: 742.  
 Location/Qualifiers

## FEATURES

source

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 /tissue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Sali;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 199 a 192 c 183 g 218 t  
 ORIGIN

Query Match 6.4%; Score 714.2; DB 10; Length 792;  
 Best Local Similarity 97.1%; Pred. No. 2.8e-145;  
 Matches 770; Conservative 0; Mismatches 18; Indels 5; Gaps 4;  
 Qy 9627 gccgggaagggcgagcggaagtgctcgtcaactttatccgctccatccagctcatt 9686  
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 Qy 9687 aattgttcgcgggaagctagagtaagtagtccagtgtaataagtttgcgaacgttgtt 9746  
 Db 61 AATTGTTGCCGGGAAGCTAGTAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTT 120

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Qy 9747 gccattgctacagggaatcgtggtgcacgctcgtcgtgttggtatggtcttcattcagctcc 9806
Db 121 GCCATTGCTTACAGGCATCGTGGTGTACAGCTCGTCG- TTGGTATGGCTTCATTCACTCC 179
Qy 9807 ggttcccaacgatacaaggcgagttacatgatcccccatgttgtaaaaaaacggttagc 9866
Db 180 GGTTCCTCAACGATCAAGCGGAGTTCATATGATCCCCCATGTGTGCAAAAAGCGGTAGC 239
Qy 9867 tcctcgggtccctccgatcgttgtcagaagtaagtgtgcccagtggttatcactcaggtt 9926
Db 240 TCCTTCGGTCCCGCATCGTGTGCAAGTAAGTGTGGCCGACGTTGTATCCTCATCGGT 299
Qy 9927 atggcagcactgcataattctcttactgtcgtccatccctgaagatgctttctgtgact 9986
Db 300 ATGGCAGCACTGCATAATTCTTCTACTGTATGCATCCGTAAGATGCTTTCTGTGACT 359
Qy 9987 ggtgaactactcaaccaagtcattcgaataagtagtattgtagcgagcgagtgctcttcg 10046
Db 360 GGTGAGTACTCAACCAAGTCATCTGAGAATAGTGTATGCGGACCGAGTTGCTCTTGC 419
Qy 10047 ccggcgtcaacacgggataataaccgcgccacatagcagaactttaaaagtgcctcatt 10106
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Qy 10107 gnaaaacgttttcggggcgaaaactctcaaggatcttcaagctgttgcagctccagttcg 10166
Db 480 GGAACACGTTCTTCGGGGCGAAACTCTCAAGGATCTTACCGGTGTGAGATCCAGTTCCG 539
Qy 10167 atgaaccacactcgtgcacccaactgatcttcagcatcttttactttcacccagctttct 10226
Db 540 ATGTAACCCACTCGTGACCCCAACTGATCTTTCAGCATCTTTTACTTTCACCAACGTTCT 599
Qy 10227 ggttgagcaaaaacagggaagcaaatccgcgaataaagggaataaggcgacacgaaa 10286
Db 600 GGGTGAGCAAAACAGAGAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAA 659
Qy 10287 tgtgaatactcatactcttcc--tttttcaatatatttgaa-gcatttatcagggttat 10343
Db 660 TGTGTAATCTCATACTCTTCCTCTTTTCCAAATATATTGAACGCAATTTATCAGCCTTAT 719
Qy 10344 tftctcatagcggtacatatattgaatgtatttagaaaaataaacaataagggttcg 10403
Db 720 TGTCATAGCGGATACATATTTGGCTGTATTTCAGAAAATACACAAATAGGGGTTCCG 779
Qy 10404 cgcacatttcccc 10416
Db 780 -GCACATTTCCCC 791

RESULT 11
AQ856202/c 757 bp DNA linear GSS 03-NOV-1999
LOCUS nbe0001F05f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
DEFINITION clone nbe0001F05f, DNA sequence.
ACCESSION AQ856202
VERSION AQ856202.1 GI:6206659
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 757)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 29
High quality sequence stop: 232.
Location/Qualifiers
1. 757
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/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbe0001F05f"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBACIndigo; Site.1: EcoRI; Site.2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa.
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
BASE COUNT 204 a 180 c 178 g 185 t 10 others
ORIGIN

Query Match 6.0%; Score 674.6; DB 12; Length 757;
Best Local Similarity 98.0%; Pred. No. 1.3e-136;
Matches 702; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

Qy 8784 ggaagctccctcgtgcgtctctctgttccgaccttcgcgttaccggatacc-tgtccgc 8842
Db 755 GAAAGCTCCTTCGTGCGCTCTCCTGTTTCNGACNTGGGCTTTACGGATACCTGTGNCG 696
Qy 8843 ctcttccc-cttcgggaagcgtggcgctttctcaatgctcacgcgttagtattcagtt 8901
Db 695 CTTTCTCCNCTTCGGAACGCTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTT 636
Qy 8902 cgtgtagctcgttcgctccaaagctgggctgtgtgcagaaaccccccgcttcagccgacc 8961
Db 635 CGGTGTAGGTTCGTTGCTCCAAAGCTGGGCTGTGTCCACGAACCCCGCTTTCAGCCGACC 576
Qy 8962 gctgcgcttattccggttaactatcgttcttgagtcacaacccggttaagacacgcttatcg 9021
Db 575 GCTGGCGCTTATCCGCTAATATCTCTTGAGTCCAACCCCGGTAAAGACACGACTTATCG 516
Qy 9022 cactgcagcagccactggtaacaggattagcagagcgaagtatgtaggcgtgctacag 9081
Db 515 CACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGGAGGTATGTAGCGCGGTGCTACAG 456
Qy 9082 agttctgaagtgggtggcctaactacgctcacactagaagacagatttgggtatctcg 9141
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Qy 9142 ctctgctgaagccagttacccttcggaaaaagagttgtagctcttgatccggcaacaaa 9201
Db 395 CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAACAA 336
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Db 335 CCACCGCTGGTAGCGGTGGTTTCTTTGCAAGCAGCAGATACGGCGCAGAAAAAAG 276
QY 9262 gatctcaagaagatcccttggatctttctacaggggtctgacgctcgaagggaacgaaact 9321
Db 275 GATCTCAAGAAAGATCCCTTGTATCTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACT 216
QY 9322 cactgtaaggatcttgatcatgagattatcaaaaaggatctccactagatccttttaa 9381
Db 215 CACGTTAAGGATTTTGGTCATGATATATCAAAAAGGATCTTCACTAGATCCCTTTTAA 156
QY 9382 attaaaaatgaagttttaaatcaatcaatgaagtatatgatgtaaaacttggtctgacagtt 9441
Db 155 ATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTTGGTCTGACAGTT 96
QY 9442 accaatgcttaatcagtgagggacclatctcagcgatctgcttatttcgttcatcc 9497
Db 95 ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTGCTTCATCC 40

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LOCUS 602826032F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954975 5',
DEFINITION mRNA sequence.
ACCESSION BG920379
VERSION BG920379.1 GI:14300855
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 754)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabps-f@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10916 row: 0 column: 08
High quality sequence start: 15
High quality sequence stop: 717.
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/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 201 a 174 c 166 g 213 t
ORIGIN

Query Match 6.0%; Score 671.6; DB 10; Length 754;
Best Local Similarity 96.3%; Pred. No. 5.7e-136;
Matches 709; Conservative 0; Mismatches 24; Indels 3; Gaps 2;

QY 9730 gtttcgcaacgttggtgcatgctacagggatcgtggtgcaagctcgctgttgta 9789
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QY 9850 gcaaaaaagcggttagctccttcgggtccctccgatcgttgtcagaagtagtgcccgag 9909
Db 131 CCAAAAAGCGGTTAGTCTCTTCGGTCCCTCCGATCGTTGTCAGAACTAAGTTGGCCGAG 190
QY 9910 tttatcaactcagttggttatggcagcaactgcataatctcttactgtcatgccatccgtaa 9969
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QY 9970 gatctttctgactggtagtactcaaccaagtcattctgagaatagtgatgcgagc 10029
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QY 10030 gaccgagttgctcttgcgcggcgctcaaacacgggataataaccgcgcacatagcgaactt 10089
Db 311 CACCGAGTTGCTCTTGCCCGCGCTCAATACGGGATAAATACCGCGCCACATAGCAAACTT 370
QY 10090 taaaagtgtctatcatctggaaaaacgttcttcggggcgaaaaactctcaaggatcctaccgc 10149
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QY 10150 tgttgagatccagttcgatgtaaccccaactcgtgcacccaactgatctcgaactcttita 10209
Db 431 TGTTGAGATCCAGTTCGATTAACCCCACTCGTGCACCCCAACTGATCTTCAGCATCTTTTA 490
QY 10210 ctttcaccagcgtttctgggtgagcaaaaacaggaaggcaaatgccgca--aaaaaggg 10267
Db 491 CTTTCAACGAGGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAACAAAGGGA 550
QY 10268 aataagggcaacacgaaatgttgaaatactactactctctcttcttcaattatttaag 10327
Db 551 ATACGGCGCAGACGGAATGTTGAATACTCATCTCTCTCTTTTCATTAATTAATGAAG 610
QY 10328 cattatcaggggttatgtctcatgagcggatcacatatatttgatgtatttgaaaaataa 10387
Db 611 CATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTAGAAAAATAA 670
QY 10388 acaaatagggttcgcg-cgcacattccccgaaagtgccacctgacgtcctaagaacca 10446
Db 671 ACAATAGGGGTTCCGCGCGACATTTCCCGRAAAGTGCCACCTAAATGTACACGGTTA 730
QY 10447 ttattatcatgacatt 10462
Db 731 ATATTTCTGTTAAAAAT 746

RESULT 13
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LOCUS AL598527 693 bp mRNA linear EST 14-AUG-2001
DEFINITION DKF2P31301920_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION DKF2P31301920 5', mRNA sequence.
VERSION AL598527
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann
,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Duesterhoeft A
MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

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Db 422 GGCTAACTACGGCTACACTAGAACACAGTATTGGTATCTGCGCTCTGCTGAAGCCAG 363  
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Db 362 TTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGCGCAAAACAAACCCACCGTGTAGCG 303  
QY 9217 gtgggtttttgttgcaagcagcagattacgcgcaaaaaaaagatctcaagaagatc 9276  
Db 302 GTGGTTTTTGTTCGAAGCAGCAGATTTACGCGCAGAAAAAAGATCTCAAGAGATC 243  
QY 9277 ctttgatctttctacggggtgctgacgctcagtggaacgaacaaactcaogttaaggattt 9336  
Db 242 CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACAAACCTCACCGTTAAGGGATT 183  
QY 9337 tggatcagagattatcaaaaaggatcttcacctagatccttttaattaaaaataagaatt 9396  
Db 182 TGGTCATGAGATTATCAAAAAGGATCTCACCTAGATCCTTTTAAATTAATAATGAAGTT 123  
QY 9397 ttaataatcaatgaatatatatagtaaaacttggtctgacaggttaccgaagtttaataca 9456  
Db 122 TTAATATCAATCTAAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCA 63  
QY 9457 gtgag 9461  
Db 62 GTGAG 58

RESULT 15  
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LOCUS AL645322 XGC-neurula Silurana tropicalis cDNA clone TNeu017h02 5',  
DEFINITION mRNA sequence.  
ACCESSION AL645322  
VERSION AL645322.1 GI:16797447  
KEYWORDS EST.  
SOURCE Silurana tropicalis  
ORGANISM western clawed frog.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Silurana.  
1 (bases 1 to 675)  
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.  
Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
JOURNAL Unpublished (2001)  
COMMENT Contact: Huckle E  
Sanger Centre  
Hinnton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TNeu017h02.sp6  
Sequencing primer: Sp6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
FEATURES  
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1..675  
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/note="Vector: pCS107; Site.1: EcoRI; Site.2: NotI; cDNA  
was oligo dT primed from 5ug of poly A+ RNA from neurula.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end."  
BASE COUNT 153 a 185 c 174 g 163 t  
ORIGIN

Query Match 5.9%; Score 656.2; DB 9; Length 675;  
Best Local Similarity 99.4%; Pred. No. 1.3e-132;  
Matches 669; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Search completed: September 21, 2002, 07:27:44  
Job time: 32958 sec

QY 8675 ggcgtttttccatagggtccgccccctgacgagcatcaaaaaatcgacgctcaagtca 8734  
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QY 8735 gggggtgcaaaacccgacagactataaagataccagcggtttccccctggaagctccct 8794  
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QY 8795 cgtgcgtctcctgttccgacccctgcggttaccggataacctgtccgcctttctcccttc 8854  
Db 123 CGTGGCTCTCTCTTCCGACCCCTGCGGCTTACCGGATACCTGTCCGGCTTCTCCCTTC 182  
QY 8855 ggaagcgtggcgctttctcaatgctcaagcttagtatactcagttcgtgtgaggtcgt 8914  
Db 183 GGGAAACGCTGGCGCTTCTCATAGCTCACGCTGAGTATCTCAGTTCTGTTAGTTCGT 242  
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Db 243 TCGCTCCAAAGCTGGGCTGTGTGACGAACCCCGCTTCAGCCCGACCGCTGCGCTTATC 302  
QY 8975 cggtaactatcgcttgcgtccaaacccggtaagacacagcttctgcgacctggcagcgc 9034  
Db 303 CGGTAACTATCGTCTTGAGTCCAACCCGGTAAACACAGCACTTATCGCCACTGGCAGCAGC 362  
QY 9035 cactggttaacagagattagcagagcgaggtatgtaggcggtgctacagagttcttgaagt 9094  
Db 363 CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTTGAAGTG 422  
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QY 9155 agttaccttcggaaaaaagagttggtagctcttgatccgcgcaaaaaacacccgctgtag 9214  
Db 483 AGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGCCAACCAACACCGCTGGTAG 542  
QY 9215 cggtaggtttttttgttgcaagcagcagattacgcgcaaaaaaaggatctcagaaga 9274  
Db 543 CGGTGGTTTTTTTGTGTTTGAAGCAGCAGATTAACGGCGCAGAAAAAAGGATCTCAAGAAGA 602  
QY 9275 tcccttgatctttctacggggtctgacgctcagtggaacgaaaaactcacgttaaggat 9334  
Db 603 TCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACAACTCACCGTTAAGGAT 662  
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Db 663 TTTGGTCAATGAGA 675





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RESULT 3  
US-09-039-641-21/c  
: Sequence 21, Application US/09039641  
: Patent No. 6251627  
: GENERAL INFORMATION:  
: APPLICANT: Cai, Zeling  
: APPLICANT: Sprent, Jonathan  
: APPLICANT: Brunmark, Anders  
: APPLICANT: Jackson, Michael

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: APPLICANT: Peterson, Per A  
: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR  
: TITLE OF INVENTION: ACTIVATION OF T-CELLS  
: NUMBER OF SEQUENCES: 45  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Olson & Hierl, Ltd.  
: STREET: 20 No. 6251627th Wacker Drive, Suite 3000  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/039,641  
: FILING DATE: 8-MAR-1995  
: CLASSIFICATION:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Olson, Arne M.  
: REGISTRATION NUMBER: 30,203  
: REFERENCE/DOCKET NUMBER: TSRI4710  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (312) 580-1180  
: TELEFAX: (312) 580-1189  
: INFORMATION FOR SEQ ID NO: 21:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 3875 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: HYPOTHEICAL: NO  
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: US-09-039-641-21
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Query Match 18.2%; Score 2034.2; DB 4; Length 3875;  
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Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY	10162	gttcgatg	taaccactcgtgc	acccaactgattctc	agcatctttac	ctttccaccagcg	10221
Db	1983	GTTCGATTAACCACT	CTGTGACCAACTGAT	CTTCAGCATCTTTTACT	TTACTTTCAC	CACGCG	1924

RESULT 4  
US-09-039-762A-21/c  
Sequence 21, Application US/09039762A  
Patent No. 6255073  
GENERAL INFORMATION:  
APPLICANT: Cai, Zeling  
APPLICANT: Sprent, Jonathan  
APPLICANT: Brunmark, Anders  
APPLICANT: Jackson, Michael  
APPLICANT: Peterson, Per A.  
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS  
TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Olsson & Hierl, Ltd.  
STREET: 20 No. 6255073th Wacker Drive, 36th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,762A  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OLSON, Arne M.  
REGISTRATION NUMBER: 30,203  
REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 580-1180



TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3875 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-762A-21

Query Match 18.2%; Score 2034.2; DB 4; Length 3875;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 8662 agttcaagaagaggcggtttttccatagdgctccgccccctgacgagcatcaaaaaatc 8721  
DB 3483 AGCGCGCTTGTGGCGTATTTCCATAGGCTCCGCCGCCCTGACGAGCATCAAAAAATC 3424  
  
QY 8722 gacgtcaagtcagagtgaggaaaccgacagagactataaagataaccagggtttcccc 8781  
DB 3423 GACGCTCAAGTCAGAGTGGCGAAACCGACAGGACTATAAAGATACAGAGCGTTTCCCC 3364  
  
QY 8782 ctggaagctccctgctgctctctctgttccgacctcgccgtctaacggatacctgtccg 8841  
DB 3363 CTGGAAGCTCCCTCGTGGCGCTCTCTGTTCGGACCCCTGCGGCTTACCGGATACCTGTCCG 3304  
  
QY 8842 cctttcccttcgggaagcgtggcgctttctctaatgctcaagctgtagtattcagtt 8901  
DB 3303 CCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAAGCTGTAGTATCTCAGTT 3244  
  
QY 8902 cggtaggtcgttcgtccaaagctggcgtgtgtgcaaaaccccggttcagccgcagc 8961  
DB 3243 CGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCCGACC 3184  
  
QY 8962 gctgcgcttaccggttaactatogtcttgagtcaccaaccggtaagacacgacttatcgc 9021  
DB 3183 GCTGCGCTTATCCGGTAACATACTGCTGTGAGTCCAAACCCGGTAAGACACGACTTATCGC 3124  
  
QY 9022 cactggcagcagcactggttaacaggaattagcagagcaggtatgtaggcgtgtctacag 9081  
DB 3123 CACTGGCAGCAGCCTGTGTAAACAGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAG 3064  
  
QY 9082 agttcttgaagtgtgcttaactacgtctacactaagaagacagttatttgtatctgcg 9141  
DB 3063 AGTCTTGAAGTGTGGCTTAACCTACGCTACACTAAGAGACAGTATTGTGTATCTCGC 3004  
  
QY 9142 ctctgctgaagccagttaccttcgaaaaaagagtgtgtagctcttgatccggcaacaaa 9201  
DB 3003 CTCTGCTGAAGCCAGTTACCTTCGAAAAAAGAGTTGTGTAGCTCTTGATCCGGCAACAAA 2944  
  
QY 9202 ccaccgctgtagcgtgtgttttttcttgcgaagcagcagattacgcgcagaaaaaag 9261  
DB 2943 CCACCGCTGTAGCGGTGTTTTTTTGTGTTCAAGCAGCAGATTAGCGCGCAGAAAAAAG 2884  
  
QY 9262 gatctaaagaatcctttgatctttctacggggtctgacgctcagtggaacgaaaaact 9321  
DB 2883 GATCTAAGAAGATCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAGCAAAAACT 2824  
  
QY 9322 caggttaagggtatttggtcatgagattatcaaaaaagatcttcaactagatcccttttaa 9381  
DB 2823 CACGTTAAGGGATTGTTGGTCATGAGATTATCAAAAAAGGATCTTCACTAGATCCCTTTAA 2764  
  
QY 9382 attaaaaaqaagtttctaaatacctaaagtatatatgagtaaaccttggtctgcagtt 9441  
DB 2763 ATTAAAAAGAGTTTAAATCAATCTAAAGTATATATAGTAAGTAACCTTGGCTGACAGTT 2704  
  
QY 9442 acaatgcttaactcaaggaagcaactatctcagcgatctgtctattctgtcatccatag 9501  
DB 2703 ACCAATGCTTAATACAGTAGGCAACCTATCTCAGCGATCTGTCTATTATTCTTCATCCATAG 2644

QY 9502 ttgcctgaactcccgctgctgtagataactaactagatacggagggtttacatctgcacca 9561  
DB 2643 TTGCTTGACTCCCGCTGCTGTGTAGATAACTACGATACGGGAGGCTTTACCATCTGCCCCA 2584  
  
QY 9562 gtgtgcaatgataccggagagaccacgctccacggctccagatttccagcaataaaacc 9621  
DB 2583 GTGCTGCAATGATACCGGAGAGACCACGCTCACGGCTCCAGATTTATCAGCAATAAAC 2524  
  
QY 9622 agccagccgaaagggccgagcgagcgaagtgtctcgaactttatccgctccatccag 9681  
DB 2523 AGCCAGCCGGAAGGGCCGAGCGCAGAGTGTCTGCAACTTTATCCGCTCCATCCAGT 2464  
  
QY 9682 ctatttaattgttcgcccgaagctagagtaagtaagtcagcagtttaattgtgcgcaacg 9741  
DB 2463 CTATTAAATTGTTGCCGGGAAGTAGAGTAAGTTAGTTCGCCAGTTAATAGTTTGCACAACG 2404  
  
QY 9742 ttgtgccattgtctacagggcatcgtgggtgcacgctcgtctgttggtatggcttcattca 9801  
DB 2403 TTGTTGCCATTGCTACAGGCAATCGTGGTGTACGCTCGTGTGGTATGGCTTTCATTCA 2344  
  
QY 9802 gctccggttcccaacgatacaaggcgagttacatgatcccccatgttgtgcaaaaaagcgg 9861  
DB 2343 GCTCCGGTTCCTCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG 2284  
  
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DB 2283 TTAGCTCCTTCGGTCTCCGATCGTGTGTCAGAAGTAAGTTGGCGCGAGTGTATTACACTCA 2224  
  
QY 9922 tgggttagggcagcactgcaataattctcttactgtcatgcatccatcgcgtaagatgctttctg 9981  
DB 2223 TGGTTATGGCAGCACTGTCATAATTCTCTTACTGTATGTCATGCCATCCGTAAAGTCTTTCTG 2164  
  
QY 9982 tgaactgtaagtaactcaaccgaagtcattctgaagaatagttatgcggcaccgagttgct 10041  
DB 2163 TGACTGCTGAGTACTCAACCAAGCTATCTTCAGAGTAAGTTGGCGCGACGAGTGTGCT 2104  
  
QY 10042 cttgcgcccggcgttaacacgggataataccgcgcacatagcagaactttaaaagtgcaca 10101  
DB 2103 CTTCGCCGCGCTCAATACGGGATAATACCGCGGCACATAGCAGAATCTTTAAAGTGTCTCA 2044  
  
QY 10102 tcaattgaaagcgtcttcggggcgaaacactctcaagatcttaccgctgttgagatcca 10161  
DB 2043 TCATTGGAAAAAGCTTCTTCGGGGCGAAAACTCTCAAGGATCTTTACCGCTGTGTGAGATCCA 1984  
  
QY 10162 gttcgtatgaacccactcgtgcacccaactgactctcagcatctttactttaccagcgcg 10221  
DB 1983 GTTCGATGTAAACCACTCTGTCACCAACTGATCTTTCAGCATCTTTTACTTTTACCCACG 1924  
  
QY 10222 ttctcgggtgagcaaaaaacaggaaggcaaaatgcgcgcaaaaaagggaataagggcgacac 10281  
DB 1923 TTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCGCAAAAAAGGAATAAGGGCGCACAC 1864  
  
QY 10282 ggaatggtgaataactcaactcttctcttcaataattattgaagcatttatcagggtt 10341  
DB 1863 GGAAATGTTGAATACTCATACTCTTCTCTTTTCAATATATTATGAAGCATTTTATCAGGCTT 1804  
  
QY 10342 attgctctatgagcgagatacatattgaatatttagaataataaataaagagttc 10401  
DB 1803 ATGTCTCATGAGCGGATACATATTGAAATGATTATGAAAAATAAACANATAGGGGTT 1744  
  
QY 10402 cgcgcacatttcccggaaagtgccacctgcagctcagctcgcgcttcggtgatgagc 10461  
DB 1743 CGCGCATTTTCCCGGAAAGTGCACCTGACGCTTAAGAAACCATTTATTATCATGAGAT 1684  
  
QY 10462 taacctataaataagcgatcagcagggccttcgctcgcgcttcggtgatgagc 10521  
DB 1683 TAACCTATAAAATAGGCGTATCAGAGGCCCTTTCGTCTCGCGCTTTTCGGTGATGAGC 1624  
  
QY 10522 gtgaaacctctgaacatgacgtcccgagagagcggtcaacagcttgtctgtaagcgagtg 10581  
DB 1623 GTGAAAAACCTCTGACACATGACGTCCCGGAGCGGTCAAGCTTCTGTGAAGCGGATG 1564  
  
QY 10582 ccgggagcagacaagcccgctcagcgcgctcagcggtgtgttgccgggtgtcgggcgtctggc 10641



Db 1563 CCGGAGACACAGCCCGTCAGGGCGCTCAGCGGGTGTGGCGGCTGGC 1504  
Qy 10642 ttaactatgaggcatcagagcagattgtactagagtgacacatatcggtgtgaaatac 10701  
Db 1503 TTAACATATGGGATCAGAGCAGATGTACTGAGAGTGACCATATGCGGTGAATAC 1444  
Qy 10702 cgcaccgaatgcgcgggaactaa 10724  
Db 1443 GGCACAGATCGGTAAGGAGAAA 1421

## RESULT 5

US-09-039-982A-27/c

: Sequence 27, Application US/09039982A

: Patent No. 6225042

: GENERAL INFORMATION:

: APPLICANT: Cai, Zeling

: APPLICANT: Sprent, Jonathan

: APPLICANT: Brunmark, Anders

: APPLICANT: Jackson, Michael

: APPLICANT: Peterson, Per A

: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CELL

: NUMBER OF SEQUENCES: 59

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Olson &amp; Hierl, Ltd.

: STREET: 20 No. 6225042th Wacker Drive, Suite 3000

: CITY: Chicago

: STATE: Illinois

: COUNTRY: USA

: ZIP: 60606

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/039,982A

: FILING DATE: 16-MAR-1998

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Olson, Arne M.

: REGISTRATION NUMBER: 30,203

: REFERENCE/DOCKET NUMBER: TSRI4710

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (312) 580-1180

: TELEFAX: (312) 580-1189

: INFORMATION FOR SEQ ID NO: 27:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3878 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: HYPOTHETICAL: NO

: ANTI-SENSE: NO

US-09-039-982A-27

Query Match 18.2%; Score 2034.2; DB 4; Length 3878;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 8662 agttcaagaagaaggctttttccatagctccgcccccccgagagcatcacaaaaac 8721  
Db 3486 AGGCGCGTGTGCGGCTTTTCCATAGGCTCCGCCCCCTCAGCAGCATCACAAAATC 3427  
Qy 8722 gacgtcaagtccagagtggtggaaccccgacaggactataaagataccagcgctttccc 8781  
Db 3426 GACGCTCAAGTCAGAGGTGGCGAACCACAGAGACTATAAGATACCAGCGCTTCCCC 3367  
Qy 8782 ctgaaagctccctcgactctctgttccgacctccgcttaccgataacctgctcg 8841

Db 3366 CTGGAAGCTCCCTCGTGGCTCTCCTGTGTCCGACCTTCGCGCTTACCGGATACCTGTCCG 3307  
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Db 3306 CTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCASTT 3247  
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Db 3246 CGGTGTAGGTGCTTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGACC 3187  
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Db 3186 GCTCGGCTTATCGGTAACTATCTGCTTGTAGTCCAAACCCGTAAGACACGACTTATCGC 3127  
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Qy 9082 agttctgaagtggtgcttaactacgctacactagaagacagatttggttatctgcg 9141  
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Qy 9142 ctctgctgaagcagttaccttcggaaaaaagattggtagctcttctgattcgcggcaacaaa 9201  
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Qy 9202 ccaccgctggtagcgtggtttttttgttgcgaagcagcagattacgcgcagaaaaaag 9261  
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Qy 9262 gatctcaagaagatcctttgatctcttctacggggtctgacgctcagtggaacgaacact 9321  
Db 2886 GATCTCAAGAAGATCCTTTTGATCTTTTTCACGGGCTCTGACGCTCAGTGGAAACAAAAC 2827  
Qy 9322 cacttaagggttttggctcatgagattatcaaaaagatcttcaacctagatcttttaa 9381  
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Db 2466 CTATTAAATGTTCGCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCAACG 2407  
Qy 9742 ttgttgcaattgcacagcatcgtgtgtacgctcgtcgttctgttgatgcttcattca 9801  
Db 2406 TTGTTGCCATGCTACAGGCATCGTGTGTACGCTCGGTGGTGGTAGGCTTCAITCA 2347  
Qy 9802 gctcgggttccccacatcaagcgaggttacatgatcccccatggttgcgcaaaaagcgg 9861  
Db 2346 GCTCCGGTTCCTCAACAGATCAAGCGGAGTTTACATGATCCCGCATGTGTGCAAAAAGCGG 2287  
Qy 9862 ttactccttcgctcgtcgttcgagtggttcagaaagtaagttaggcagcaggtgttactca 9921  
Db 2286 TTAGTCTCTCGGCTCCGATCGTTGTGTAAGTAAGTTGGCCCGCAGTGTATCACTCA 2227





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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-039-762A-27

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Query Match 18.2%; Score 2034.2; DB 4; Length 3878;  
Best Local Similarity 99.1%; Pred. NO. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY	8662	agttcaagaagaaggcgtttttccatagctgcgccccctgacagagcatcacaaaaac	87821
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QY	8722	gacgtcaagtcagaggtgacgaaccgacagagactataaagataccaggcgtttcccc	8781
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QY	8782	ctggaagctccctcgtgcgctcctctgttccgcacctgccgttaccggaTaccctgtccg	8841
Db	3366	CTGGAAGCTCCCTCGTCGCTCTCCTGTTCCGACCTGCCGCTACCGGATACCTGTCCG	3307
QY	8842	cttttcccttcgggaagcgtggcgcttctcgaatgcacgctgtaggtatcagtt	8901
Db	3306	CCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTACGCTGTAGGTATCTCAGTT	3247
QY	8902	cgggtaggtcgtctgcgtccaaagctggcgctgtgtgcacgaacccccggttcagccgacc	8961
Db	3246	CGGTGTAGTCTGCTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCCCGTTTCAGCCGACC	3187
QY	8962	gctgcgcttataccggttaactcgtctgagtcacaccccggttaagacacgaacttatcgc	9021
Db	3186	GCTGCGCCTTATCCGGTAACTATCTGCTTTGAGTGCACCCCGTAAGACACGACTTATCGC	3127
QY	9022	cactggcagaccactgataacagattacaagacgaggtatgtaggcgggtgctacag	9081
Db	3126	CAC TGCCACACGCCACTGATAACAGATTACGAGGCGAGGATGTAGGCGGTGCATACAG	3067
QY	9082	agttctgaagtggtggcctaactacgcgtacactagaagacagattttgggtatctgcg	9141
Db	3066	AGTTCTTGAAGTGGTGGCTAACTACGCGCTACACTAGAAGGACAGTATTGGTATCTGCG	3007
QY	9142	ctctgctgaagccagttaccttcctcggaataaagagtgtgtagctcttgatccgggcaacaaa	9201
Db	3006	CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTGTGTAGCTCTGTATCGCGCAACAAA	2947
QY	9202	ccaccgctgtagcgggtgggtttttgtttgcaagcagcagattacgcgcagaaaaaaag	9261
Db	2946	CCACCCTGGTAGCCGTGGTTTTTTTGTTCGACAGCAGCAGATTACCGCGAGAAAAAAG	2887
QY	9262	gatctcaagaagatcctttgatctttctacggggtgcgcgtcagtgaaacgaaacact	9321
Db	2886	GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGTACGCTCAGTGAACGAAAACT	2827
QY	9322	cacgttaagggaatttgcctgatgattataaaaggatcttcaoctagatccttttaa	9381
Db	2826	CAGGTTAAGGATTTTGGTCATGAGATTATCAAAAGAGTCTTACCATAGATCCTTTTAA	2767
QY	9382	attaaaaatgaagtttttaaatcaatctaaagtatatatgagtaaaacttgctgcagtt	9441
Db	2766	ATTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGCAGATT	2707
QY	9442	accaatgcttaactcagtgaggcaacctatctcagcgatctgtctatttgcgttcaatag	9501
Db	2706	ACCAATGCTTAATCAGTCAGACGACTATCTCAGCGATCTCTCTATTTCGTTTCATCCATAG	2647
QY	9502	ttgcctgactcccgctcgtgtagataactacgaTaccggaggcgttaccatctggcccca	9561
Db	2646	TTGCGCTGACTCCCGTCGTGTAGATACTACGATACGGGAGGCGTTTACCATCTGGCCCCA	2587
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Db	2586	GTGCTCGAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAACC	2522
Qy	9622	agcagccggaagggccgagcgagagaagtggctctgcaactttatccgcctccatccagt	9681
Db	2526	AGCCAGCGGAAGGGCCGAGCGAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGT	2467
Qy	9682	ctattaattggtgcgggaagctagagtaagttagttcgccagtttaatatgtttgcgcaacg	9741
Db	2466	CYATTAATTTGTTCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGCTTTTCGCAAG	2407
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Qy	9802	gtccgggttccaaagatcaagcgagttacatgatcccccatgttgtgcacaaaagcgg	9861
Db	2346	GCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTCAAAAAGCGG	2287
Qy	9862	ttagctcttcggtccctcgatcggtgttcagaaagtaagtggccgcagtggttatcactca	9922
Db	2286	TTAGTCTCTTCGGTCTCCGATCGTTGTTCAGAAGTAAGTTGGCCGACGTTTATCACTCA	2227
Qy	9922	tgtttatggcagcactgcataaattcttctactgtcatgcataccctgaagatcgtttctg	9981
Db	2226	TGGTTATGCGACACTGCAATAATCTCTTACTGTCAATGCCATCCGTFAAGATGCTTTCTG	2167
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Qy	10042	cttgcggcggtcaacacgggataataccgcgcacatagcagaactttaaaagtgctca	10101
Db	2106	CTTGGCCGCGCTCAATACGGGATATACCGGCCACATAGCAGAACTTTAAAGTGCTCA	2047
Qy	10102	tcattgaaaaactcttcggggcgaaaaactctcaaggatcttaaccgctgttgagatcca	10161
Db	2046	TCATTGGAAAGGTTCTTCGGGGCGGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCA	1987
Qy	10162	gttcgatgaacccaactcgtgcacccaactgatcttcagcatctttactttccaccagcg	10221
Db	1986	GTTTCGATGTAAACCACTCGTGCCACCACTGATCTTTCAGCATCTTTTACTTTCCACGCG	1927
Qy	10222	ttcttggtgagcaaaacaggaagcgaaaaatgcgcacaaaaggaataaagggcgacac	10281
Db	1926	TTTCTGGGTGAGCAAAAACAGGAAGCAAAATGCCGCAAAAAGGGAATAAGGGCGACAC	1867
Qy	10282	ggaatggtgaactcaactcttcctttttcaatatattgaagcaatttatcagggtt	10341
Db	1866	GAAATGTTGAATACTCATACTCTTCCTTTTTCATATATTATGAAGCATTTATCAGGGTT	1807
Qy	10342	attgtctcatgagcggatcacattattggaatgtatttagaaaaataacaaataggggttc	10401
Db	1806	ATTGTCTCATGAGCGGATACATATTTTGAATGTAATTTAGAAAAATAACAATAGGGTTTC	1747
Qy	10402	cgcgcacatttcccgaataagtgcacctgcgctcgttaagaacaattattcatgacat	10461
Db	1746	CGCGCACATTTCCCGGAAAATGCCACTGACCTGCTAAGAAACCATTTATTCATGAGAT	1687
Qy	10462	taacctataaaaaataggggtatcacagggcccttctcgcgcgcttcggtgatgacg	10521
Db	1686	TAACCTATAAAAATAGGGGTATCAGGAGGCCCTTTTCGTCTCGCGGTTTCGGTGATGACG	1627
Qy	10522	gtgaaaacctctgacacatgcagctcccgagagcgggtcacagcttgtgtgtaagcgatg	10581
Db	1626	GTGAAAACCTCTGACATGACAGCTCCCGGAGCGGTCACAGCTTGCTGTGTAAAGCGGATG	1567
Qy	10582	ccggagcagacaaagccgctcagggcgctcagcggtgttgccggtgttcgggctggc	10641
Db	1566	CCGGGACGACACAGCCGCTCAGGGCGGTCAGCGGGTGTGCGGGGTGTCGGGGCTGGC	1507
Qy	10642	ttaaactatgcccacagacagattgtactgagatgacacatcgtcgggtgtgaaataac	10701
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[illegible]

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QY 10042 ctggccggcgctcaacacgggataataccgcccacatagcagaactttaaaagtgtca 10101
Db 2111 CTGCGCGCGGTCAATACCGGATAATACCGGCCACATAGCAGAACTTTAAAGTGTCTCA 2052
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Db 2051 TCATTGGAACAGTCTTCTCGGGCGGAATACTCTCAAGGATCTTACCGCTGTGAGATCCA 1992
QY 10162 gttcgtatgaacccactcgcacccaaactgattcttcagcatctttactttaccacagcg 10221
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QY 10342 attgtctcagcgagatacatatttgatgtatttagaaaaataaacaataaggggttc 10401
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Db 1691 TAACTATAAAAAATAGGGGTATCAGAGGGCCCTTTCTGCTCGCGGTTTCGCTGATGACG 1632
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QY 10702 cgcaccgaatcgcgcggaactaa 10724
Db 1451 CGCACAGATCGTGAAGGAGAAA 1429
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RESULT 9
US-09-039-641-30/c
: Sequence 30, Application US/09039641
: Patent No. 6251627
: GENERAL INFORMATION:
: APPLICANT: Cai, Zeling
: APPLICANT: Sprent, Jonathan
: APPLICANT: Brunmark, Anders
: APPLICANT: Jackson, Michael
: APPLICANT: Peterson, Per A
: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
: ACTIVATION OF T-CELLS
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Olson & Hierl, Ltd.
: STREET: 20 No. 6251627th Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 8-MAR-1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Olson, Arne M.
: REGISTRATION NUMBER: 30,203
: REFERENCE/DOCKET NUMBER: TSRI4710
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 580-1180
: TELEFAX: (312) 580-1189
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3883 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-09-039-641-30
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Query Match 18.2%; Score 2034.2; DB 4; Length 3883;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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QY 10462 taacctataaaatagcgctatcacagggcccttctcgcgcgtttcgggtgtagcag 10521  
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QY 10702 cgcacggaatcgcggaactaa 10724  
Db 1451 CGCACAGATCGCTAAGGAGAAAA 1429

RESULT 10  
US-09-039-762A-30/c  
; Sequence 30, Application US/09039762A  
; Patent No. 6255073  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zelling  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A.  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS  
; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,762A  
; FILING DATE: 16-Mar-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLSON, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3883 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-09-039-762A-30



Query Match					18.2%; Score 2034.2; DB 4; Length 3883;				
Best Local Similarity					99.1%; Pred. No. 0;				
Matches 2045; Conservative					0; Mismatches 18; Indels 0; Gaps 0;				
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Db	3251	CGGCTAGGTGCTTCCGCTCAAGCTGGCTGTGTGCAGCAACCCCTCCCTTCAGCCCGACC	3192						
Qy	8962	gctgccttatccggttaactatcgtcttgagtccaacccgtaagacacacacttatcgc	9021						
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Qy	9322	cacgttaagggttttgggtcatgagattatcaaaaggatcttccactagatccttttaa	9381						
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Qy	9502	ttgcctgaactccccctgtgtgtagataactacgatacgggaggggttaacctgtggcccca	9561						
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Qy	9682	ctattaattgttccgggaagctagagtaagtagttccaggttaagttttgcgaacg	9741						
Db	2471	CUATTAATTTGTCGGGAAGCTAGATAGTATGTTCCGACGTTAATAGTTTTCGCCACG	2412						
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Qy	9802	gctccggttcccaacagatcaagcagagttacatgatcccccatgttgtcaaaaaagcgg	9861						
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Qy	9862	ttagtcctcttggtctccgcatcgtgttcagaagtaagtggccgcgagtttatcaactca	9921						
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Qy	10462	taacctataaaaa tagcggtatcacagggcccttctgcgcggtttcgggtgatgacg	10521						
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Qy	10522	gtgaaaaacctctgacacatgcagctcccgagagcgtcacagcttctgtlaagcggatg	10581						
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RESULT 12  
US-09-039-641-24/c  
; Sequence 24, Application US/09039641  
; Patent No. 6251627  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brummark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR  
; TITLE OF INVENTION: ACTIVATION OF T-CELLS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6251627th Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039, 641

; FILING DATE: 8-MAR-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olson, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI4710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3908 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-09-039-641-24  
  
Query Match 18.2% Score 2034.2; DB 4; Length 3908;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 8662 agttcaagaagaagcggtttttccataggtccgcccccttcacagagatcaaaaaatc 8721  
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QY 8722 gacgtcaagtacagagtgccgaacccgacagagactataaagataccaggggtttccccc 8781  
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QY 8842 cettctcccttcgggaagcggttttccatagctcagcgtgtaggtatctcagtt 8901  
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Db 2916 GATCTCAAGAAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACAGAAAACT 2857  
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QY 9562 gtgctgaatataccgcgaacccacgctcaccgctccagatttatcagcaataaacc 9621  
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Db 2376 GCTCCGGTTCACACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG 2317  
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QY 9982 tgactgggtgagtactcaaccaagtcattctgagaatagtgatgcggcagcgagtgct 10041  
Db 2196 TGACTGGTGAGTACTCAACCAAGTCAATCTGAGAATAGTGTATGGCGGACCGAGTTGCT 2137  
QY 10042 cttgcccggcgctcaacacgggataataccggccacatagcagaactttaaaagtgcctca 10101  
Db 2136 CTTGCCGGCGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTAAAGTGCTCA 2077  
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Db 2076 TCATTGGAAAACGTTCTCGGGGCGCAAACTCTCAAGGATCTTACCGCTGTGAGATCCA 2017  
QY 10162 gttcagtgtaacccactogtgcacccaaactgactctcagcatcttttacttttccaccagcg 10221  
Db 2016 GTTCGATGTAACCCACTCGTGCACCACTGATCTTCAGCATCTTTACTTTTCACACCG 1957  
QY 10222 ttcttggtgagcaaaaaacagaaagcgaatgcccgaataaggaaggaagcgcacac 10281  
Db 1956 TTCTGGGTGAGCAAAAACAGGAGCAAAATGCCGCAAAAAGGAATAAGGGCGACAC 1897  
QY 10282 ggaattgtgaatactcatactcttctcttttcaatatattattgaagcatttatcagggtt 10341  
Db 1896 GGAATGTTGAATACTACTCTCTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTT 1837  
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Db 1776 CGCGACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATATTATTATCATGACAT 1717  
QY 10462 taacctataaaataggcgtatatacagagagcccttctgctcgcgcttccgltgatgacg 10521

Db 1716 TAACCTATAAAAATAGCGGTATCACGAGCCCTTTCGTCTCGCGCTTCGTGATGACG 1657  
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RESULT 13  
US-09-039-762A-24/c  
; Sequence 24, Application US/09039762A  
; Patent No. 6255073  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zelling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A.  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS  
; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,762A  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLSON, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3908 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-762A-24  
Query Match 18.2%; Score 2034.2; DB 4; Length 3908;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 2256 TGGTTATGGCAGCAGTCGATAATTCCTTACTGTCTATGCCATCCGTAAAGATGCTTTCTG 2197  
Qy 9982 tgaactgtagtactcaaccaagtcatctctgagaatagtgtatgcggcgaccaggttgc 10041  
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Qy 10582 ccgggagcagacaagccccctcagggcggtcagcggtgttggcggtgtcgtcggggtgcgc 10641  
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Db 1476 CGCAGATGCGGTAGGAGAAAA 1454

RESULT 14

US-09-194-285-7/c  
; Sequence 7, Application US/09194285  
; Patent No. 6355479  
; GENERAL INFORMATION:  
; APPLICANT: Webb, Susan R.

; APPLICANT: Wingvist, Ola  
; APPLICANT: Karlsson, Lars  
; APPLICANT: Jackson, Michael R.  
; APPLICANT: Peterson, Per A.  
; TITLE OF INVENTION: MHC Class II Antigen Presenting Systems  
; TITLE OF INVENTION: and Methods for Activating CD4+ T Cells  
; FILE REFERENCE: TSRI 536.1  
; CURRENT APPLICATION NUMBER: US/09/194,285  
; CURRENT FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: PCT/US97/08697  
; PRIOR FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: US 60/018,175  
; PRIOR FILING DATE: 1996-05-23  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 4713  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-09-194-285-7

Query Match 18.2%; Score 2034.2; DB 4; Length 4713;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 8662 agttaaagaagagcggttttccataggtccgccccccctgaagcagatcacaaaaatc 8721  
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DB 3480 TTGCTGACTCCCGCTGCTGTAGATAACTACGATACGGAGGGCTTACCATCTGGGCCCA 3421  
QY 9562 gtgctcaatgataccgcgagaccacgctccacggctccagatcttccagcaataaacc 9621  
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QY 9622 agccagccggaagggccgagcgcagaagtggtcctgcaactttatccgcctccatccagt 9681  
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QY 9802 gctccggttcccaacgatcaaggcgagttacatgatcccccatgtgtgcaaaaaagcgg 9861  
DB 3180 GCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGG 3121  
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DB 3120 TTAGTCTCCTTCGGTCCCGGATCGTTGTCAAGTAAGTTGGCCGCGAGTGTATCACTCA 3061  
QY 9922 tgggtatggcagcactgataaattctcttactgtcatgccatccgtgaagatgctttctg 9981  
DB 3060 TGGTTATGGCAGACTGCATAAATTCCTTACTGTCTATGCCATCCGTAAGATGCTTTTCG 3001  
QY 9982 tgactgtgagtactcaaccaagtcattctgagaatagttatgcgcgacccaggttgcct 10041  
DB 3000 TGACTGTGTAGTACTCAACCAAGTCATTCTGAGAATAGTGTATCGCGCACCGAGTGTCT 2941  
QY 10042 cttcccggtcgaacacgagataataacgcgcacacatagcagaactttaaaagtgcctca 10101  
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QY 10282 ggaatgttgtaatactactcttccttttccaatattattgaagcatttatcagggtt 10341  
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DB 2640 ATTGTCTCATGACGGATACATATTGTAATGTATTAGAAAAATAACAAATAGGGGTTC 2581  
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QY 10522 gtgaaacctctgacacatgcagctcccgagacggtcacagcttctgctgaagcggatg 10581
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QY 10582 ccgggagcagacaaagcccgctcaggcgcggtcagcggtgttggggggtgtcggggctggc 10641
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RESULT 15
US-09-194-285-8/c
; Sequence 8, Application US/09194285
; Patent No.. 6355479
; GENERAL INFORMATION:
; APPLICANT: Webb, Susan R.
; APPLICANT: Winqvist, Ola
; APPLICANT: Karlsson, Lars
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: MHC Class II Antigen Presenting Systems
; FILE OF INVENTION: and Methods for Activating CD4+ T Cells
; FILE REFERENCE: TSRI 536.1
; CURRENT APPLICATION NUMBER: US/09/194.285
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: PCT/US97/08697
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 60/018,175
; PRIOR FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-194-285-8

Query Match 18.28; Score 2034.2; DB 4; Length 4724;
Best Local Similarity 99.18; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 8902 cgggtgtaggtggttcgctccaagctgggctgtgtgcacgaaccccccggttcagccgacc 8961
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Db 2831 GTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCACGCG 2772
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Qy 10342 attgtctcatgagcggtacacattatttgaaatgtatttgaaaaataaacaataagggttc 10401
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Db 2291 CGCACAGATGCGTAGGAGAAA 2269
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: September 20, 2002, 22:51:11 : Search time 1531.18 Seconds  
(without alignments)  
12565.305 Million cell updates/sec  
Title: US-09-700-843-1  
Perfect score: 11206  
Sequence: 1 catgatgaataacataagg.....cacgatgagaatgccacagc 11206  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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SUMMARIES				Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	11206	100.0	11206	21	AAZ47807	Vector for trapping	
2	2628.4	23.5	2646	15	AAQ61607	Mutated GAL4 gene	
3	2439.6	21.8	7869	23	ABL05134	Drosophila melanog	
4	2102.8	18.8	7286	20	AXS57224	WO 9923223 Seq ID	
5	2034.2	18.2	3753	24	ABA04129	Plasmid pHC19T(II)	
6	2034.2	18.2	3755	24	ABA04130	Plasmid pHC19T(II)	
7	2034.2	18.2	4713	19	AAV12067	Murine IAD alpha c	
8	2034.2	18.2	4724	19	AAV12068	Murine IAD beta ch	
9	2034.2	18.2	4776	20	AAZ77617	Expression constru	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	2034.2	18.2	4776	20	AAZ77614	Expression constru
11	2034.2	18.2	5323	17	AAZ13390	Hybrid vector pSF1
12	2034.2	18.2	5364	17	AAZ13393	Hybrid vector pM1
13	2034.2	18.2	5374	21	AAZ60706	Primers attached v
14	2034.2	18.2	5421	21	AAZ68299	SV40/APPA plasmid
15	2034.2	18.2	5462	21	AAZ60707	Primers attached v
16	2034.2	18.2	5465	20	AAZ20088	Plasmid pUBTAc. C
17	2034.2	18.2	5639	20	AAZ57972	Recombinant DNA ve
18	2034.2	18.2	5897	20	AAZ63741	Plasmid pTGP190-1
19	2034.2	18.2	5932	21	AAZ45928	Nucleotide sequenc
20	2034.2	18.2	6116	21	AAZ68297	R15/APPA plasmid c
21	2034.2	18.2	6142	21	AAZ45932	Nucleotide sequenc
22	2034.2	18.2	6142	21	AAZ45933	Nucleotide sequenc
23	2034.2	18.2	6253	20	AAZ08454	AAV vector sequenc
24	2034.2	18.2	6280	20	AAZ08455	AAV vector sequenc
25	2034.2	18.2	6280	20	AAZ08456	AAV vector sequenc
26	2034.2	18.2	6565	21	AAZ45925	Nucleotide sequenc
27	2034.2	18.2	6565	22	AAZ5126	Nucleotide sequenc
28	2034.2	18.2	6708	21	AAZ68295	R15/APPA plasmid c
29	2034.2	18.2	6714	21	AAZ45930	Nucleotide sequenc
30	2034.2	18.2	6898	20	AAZ63742	Plasmid UGP232-4 c
31	2034.2	18.2	6924	21	AAZ45934	Nucleotide sequenc
32	2034.2	18.2	6924	21	AAZ45935	Nucleotide sequenc
33	2034.2	18.2	6971	22	AAZ5124	Nucleotide sequenc
34	2034.2	18.2	6981	21	AAZ45931	Nucleotide sequenc
35	2034.2	18.2	7054	21	AAZ45927	Nucleotide sequenc
36	2034.2	18.2	7405	21	AAZ45926	Nucleotide sequenc
37	2034.2	18.2	7492	21	AAZ45929	Nucleotide sequenc
38	2034.2	18.2	7558	22	AAZ5125	Nucleotide sequenc
39	2034.2	18.2	7566	14	AAQ42160	Plasmid pPS0212 co
40	2034.2	18.2	7639	14	AAQ42159	Plasmid pJD884 con
41	2034.2	18.2	7914	22	AAZ4648	Plasmid DLZ7 encod
42	2034.2	18.2	7944	22	AAZ4647	Plasmid DLZ6 encod
43	2034.2	18.2	7969	22	AAZ5123	Nucleotide sequenc
44	2034.2	18.2	8630	21	AAZ24041	Retroviral M4 mdr-
45	2034.2	18.2	8630	21	AAZ24042	Retroviral vector

ALIGNMENTS

RESULT 1

AAZ47807  
ID AAZ47807 standard; DNA; 11206 BP.

AC AAZ47807;

DT 10-MAR-2000 (first entry)

XX Vector for trapping an unknown gene of Drosophila melanogaster.

DE Gene trapping; Drosophila melanogaster; cloning; functional analysis;

DE KW artificial consensus splicing acceptor site; reporter gene;

DE KW drug resistance gene; detection; splicing donor site; ss.

OS Synthetic.

OS Drosophila melanogaster.

PN WO9961604-A2.

PD 02-DEC-1999.

PF 21-MAY-1999; 99WO-JP02683.

PR 22-MAY-1998; 98JP-0141952.

XX (NTSC-) JAPAN SCI & TECHNOLOGY CORP.

PI Lukacovich T, Asztalos Z, Yamamoto D, Awano W;

DR WPI; 2000-062708/05.

XX New gene trapping vector for Drosophila melanogaster genes, used for

the cloning and functional analysis of novel genes -  
Claim 4: Page 15-21; 35pp; English.

The present sequence represents the nucleotide sequence of a specifically claimed vector for trapping an unknown gene of *Drosophila melanogaster* (DM), where the vector is a recombinant plasmid comprising the following nucleotide sequences in order: (1) an artificial consensus splicing acceptor site; (2) a synthetic stop/start sequence; (3) a reporter gene; (4) a drug resistance gene; (5) a gene responsible for a detectable CC phenotype of the DM; and (6) a synthetic splicing donor site. The vector can be used for the cloning and functional analysis of new genes of DM.

XX  
SQ Sequence 11206 BP: 2998 A; 2648 C; 2564 G; 2996 T; 0 other;

Query Match 100.0%; Score 11206; DB 21; Length 11206;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 11206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 caataagtcgagtgaaaggaaatagattctgagtcgctgattgagtcgagtgagacag 120  
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DB 61 caataagtcgagtgaaaggaaatagattctgagtcgctgattgagtcgagtgagacag 120  
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DB 121 cgatatgattgtgattaaccttagcatgtccgctggtggttgaattaaactcataatt 180  
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QY 361 caagtcgtcgaagaacaactggaggtgcgtactctcccaaaacccaagaaggtctccgct 420  
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DB 421 gactaggcacatctgcagagaagtgggaatcaaggctagaagaactggaacagctatttct 480  
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QY 541 aaagcattgttaacagagattatttgacagaataaagtgaataaagatgcccgtcacaga 600  
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DB 541 aaagcattgttaacagagattatttgacagaataaagtgaataaagatgcccgtcacaga 600  
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AC AC
XX XX
XX XX
DT DT
XX XX
DE DE
XX XX
KW Mutated GAL4 gene coding for Asp insertion between Asp863 and Val864.
KW Mutated GAL4; heterologous gene expression; enhanced; increased;
KW protein production; positive regulator; transcription activator;
KW galactose metabolism; ss.
XX XX
OS Eukaryota.
XX XX
FH FH
FT mat_peptide Location/Qualifiers
FT 1..2646
FT /*tag= a
FT /product= mutated_GAL4
FT /transl_except= (pos:190..192, aa:Lys)
FT /transl_except= (pos:757..759, aa:Ser)
FT /transl_except= (pos:1375..1377, aa:Glu)
FT /transl_except= (pos:1990..1992, aa:Cys)
XX XX
PN JP06078767-A.
XX XX
PD 22-MAR-1994.
XX XX
PE 07-SEP-1992; 92JP-0262723.
XX XX
PR 07-SEP-1992; 92JP-0262723.
XX XX
PA (GREC ) GREEN CROSS CORP.

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XX WPI: 1994-131274/16.
DR P-PSDB; AAR51930.
XX Mutated GAL4 and a method for the expression of foreign protein -
PT useful for enhancing expression of protein
XX Claim 2; Page 13-14; 20pp; Japanese.
XX This DNA sequence codes for GAL4 in which an Asp residue is inserted
CC between wild-type Asp863 and Val864. The mutated GAL4 can be used
CC for increasing the expression of foreign genes under the control of
XX the GAL1, GAL7 or GAL10 promoters.
XX Sequence 2646 BP; 825 A; 583 C; 498 G; 740 T; 0 other;
SQ

Query Match 23.5%; Score 2628.4; DB 15; Length 2646;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2642; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 275 atgaagctactgtctctatcgaaacagcatcgatatttgcgacttaaaaaagctcaag 334
Db 1 atgaagctactgtctctatcgaaacagcatcgatatttgcgacttaaaaaagctcaag 60
QY 335 tgcctcaaaagaaacccgaaagtcgccaagtgtctgaagaacaaactggagtgctgtac 394
Db 61 tgcctcaaaagaaacccgaaagtcgccaagtgtctgaagaacaaactggagtgctgtac 120
QY 395 tctccaaaaccacaaaggtctcgcgtactagggcacatctgcacagaagtggatcaagg 454
Db 121 tctccaaaaccacaaaggtctcgcgtactagggcacatctgcacagaagtggatcaagg 180
QY 455 ctgaagaagactggaaacagctatttctactgatttttctcgcagaagacctgacatgatt 514
Db 181 ctgaagaagactggaaacagctatttctactgatttttctcgcagaagacctgacatgatt 240
QY 515 ttgaaaatgattctttacagatatataaacatgttgaacagattatttggtaacaagat 574
Db 241 ttgaaaatgattctttacagatatataaacatgttgaacagattatttggtaacaagat 300
QY 575 aatgtgaataaagatgccgtcacagatagattggcttcagtggaactgatatgcctcta 634
Db 301 aatgtgaataaagatgccgtcacagatagattggcttcagtggaactgatatgcctcta 360
QY 635 acattgagacagcatagaataaagtcgacatcatcatcggaagagtagtaacaaaggt 694
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Db 661 gttacaacaggtcccgaccatgattacgtagatatacagtttggcttctagatccacaaca 720
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QY	1115	atccttttaactgcataatagccattggagcctggtgtatagagggggaattctactgat	1174
Db	841	atcctttttaactgcaataatagccattggagcctggtgtatagagggggggaattctactgat	900
QY	1175	atagatgttttttactatcaaaatgctaatactcatttgacgacgaaggcttcgagtcga	1234
Db	901	atagatgttttttactatcaaaatgctaatactcatttgacgacgaaggcttcgagtcga	960
QY	1235	ggttcacataatttgggtgacagccctacatctctctgcgcgatatcacacagtggaagcag	1294
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QY	1895	tatgaagttaaacgatgtctccatcattgttaagcgtatgcagacaaaagaactgttatgct	1954
Db	1621	tatgaagttaaacgatgtctccatcattgttaagcgtatgcagacaaaagaactgttatgct	1680
QY	1955	gtaagtgcctatatgacaaatcataatgtccaccacataatttgcctggaaattgttcttat	2014
Db	1681	gtaagtgcctatatgacaaatcataatgtccaccacataatttgcctggaaattgttcttat	1740
QY	2015	tactgttcaatgcagctccttagtaccctataaagacttactctcaactcaaaatcgaaat	2074
Db	1741	tactgttcaatgcagctccttagtaccctataaagacttactctcaactcaaaatcgaaat	1800
QY	2075	gctgagaataacgagaccgcacaaattattacaacaaataaacactgttctgtagctatta	2134
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QY	2135	aaaaaactgcgaacttttaaaatccagacttgtgaaaaatacatctcaagtactgtagaag	2194

Db	1861	 aaaaactggccacttttaaaatccagacttggaaaaatacattcaagtactggaagag	1920
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Db	1981	aatagtaattggtagccattaaaaataattgcggtttctgcaactatgcccaataccct	2040
Qy	2315	actctccgagagaataatgtcaacaatacagtggttaataatgtttctccctggctcagta	2374
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Qy	2375	gggcttcaactgtgcattgaaatcaggagcaagtttcagtgactagtcaagctgta	2434
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Qy	2435	tctaacogtccacccctcgttaactctcagtgacaataccaagaagcacaccttcgcat	2494
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Db	2521	acggaccacaaactcgtataacgcggtttggaaatcactacagggagtgttaatacaccactaca	2580
Qy	2855	atg-- -gatgatataactatctcattcgatgatgaagatccccaccacaaacccaaaa	2911
Db	2581	atg-- -gatgatataactatctcattcgatgatgaagatccccaccacaaacccaaaa	2640
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Db	2641	aaagag 2646	

RESULT	3	
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ID	ABL05134	standard; cDNA; 7859 bp.
XX		
AC	ABL05134;	
XX		
DT	26-MAR-2002	(first entry)
XX		
DE	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 9884.
XX		
KW	Drosophila;	developmental biology; cell signalling; insecticide;
KW	pharmaceutical;	gene; ss.
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	





Qy	7357	tittcaatgaagatgatagtttattagtttttgcagaaaaataaataatttcatttaactcg	7416
Db	2046	TTTTCAATGAGATGATAGTTTATAGTTTTCGACGAAGATAAATAAATTTCAATTTAACTCG	1987
Qy	7417	cgaacatgttgaagatagaataataatgaatgcgagtaacattttaaatttcagatgg	7476
Db	1986	C-----GAATATTAATGAGATCGAGTAACATTTTATTTAATTTGCAGATGG	1944
Qy	7477	ttgccatcttgatggcctcatcttttggcccaagaacatcaogaaagtggcgctgatga	7536
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Qy	7537	atatcaacggagccatcttctctcttcagcaacaatgaccttcaaaacgctctttgccca	7596
Db	1883	ATATCAACGGAGCCATCTTCCTCTCTGACCAACATGACCTTCAAAAACGCTTTTGCCA	1824
Qy	7597	cataaaatgaagcttggtttagaatacatitgcataataataatttaactaactttcaa	7656
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Qy	7957	cgcgcggttatcaaccattcctgcttctggcgctctcttgaacttcgggctcggtg	8016
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Qy	8017	ccagtaacctcaaatgggtgtgtacctctcaatggttccgttaacgcaacagggctgtg	8076
Db	1403	CCAGTATACCTCAAAATGGTGTGTGCTACCTCTCATTTGGTTACGCCAACGAGGGTCTG	1344
Qy	8077	ctgattaaccaatgggcgagctggagccggcgaaaattagctgcacatcgtcgaaacacc	8136
Db	1343	CTGATTAAACCAATGGCGAGCTGGAGCCGGCGGCAAAATTAGCTGCACATCGTCGAACACC	1284
Qy	8137	acgtgcccaagtctcgggcaagtgcatcctcgtgagacgcttaacttctccgcgcgcgatctg	8196
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Qy	8197	ccgctggactacgtgggtctggccattctctcactgtgagcttcggggtgctgcatactg	8256
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XX	AAx57224;	
AC		
XX	26-JUL-1999 (first entry)	
XX		
XX	WO 9923223 seq ID 2.	
DE		
XX		
KW	Inducible promoter; invertase; catabolite inhibition; vector;	
XX	extracellular expression; foreign gene; regulation expression; ss.	
XX		
OS	Schizosaccharomyces pombe.	
XX		
PN	WO9923223-A1.	
XX		
PD	14-MAY-1999.	
XX		
XX	30-OCT-1998; 98WO-JP04929.	
PF		
XX		
XX	31-OCT-1997; 97JP-0314608.	
PR		
XX		
XX	(ASAG ) ASahi GLASS CO LTD.	
PA		
XX		
PI	Hama Y, Kumagai H, Tohda H;	
XX		
XX	WPI; 1999-313344/26.	
XX		
PT	Promoter and secretory signal sequences from invertase gene of	
XX	Schizosaccharomyces pombe	
XX		
PS	Disclosure; Page 52-57; 67pp; Japanese.	
XX		
CC	This invention describes a novel promoter region of the moiety relating	
CC	to catabolite inhibition of the invertase gene of Schizosaccharomyces	
CC	pombe. The products of the invention can be used in the construction of	
CC	a vector which allows extracellular expression of a foreign gene,	
CC	regulated by the presence or absence of a specific nutrient such as	
CC	glucose and results in the easy regulated expression of foreign genes	
CC	in a yeast system.	
XX		
XX	Sequence 7286 BP; 2181 A; 1557 C; 1544 G; 2004 T; 0 other;	



Db 2765 atttggttttaagaagcaccaccactctgttaaaactcttcaattctcatlagcaaggac 2824  
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Db 2825 cctttcaatctctctctttagaactcttcaattataacgaattggataatcgcgaaa 2884  
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Qy 7853 tcaactgcctggcgtgctcactctggtggccaatggtcaacgtcctcg----- 7903  
Db 4561 caatacatgagaagatgctatgtagtgaaataaaaaatgaactcaacaagacaaaaaa 4620  
Qy 7904 -----gatactcaatactcgcgcagctcctgcacctcgtgcgtgctgtgtg 7953  
Db 4621 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 4680  
Qy 7954 ggtcgcggtttatcatcaccattctcgtcttggcggtcttcttgaactcgggctcg 8013  
Db 4681 cctctgagcggaagaaacacgcggtatccagacatgataagatacattgatgattg 4740  
Qy 8014 gtgccagttacataatggtgtgcacctcgtatcctcgtatcgttccgttaacgcaaggggt 8073  
Db 4741 gaaaaaccacactagaatgcagtgaaaaaaatgcctttatttgtgaaaattgtgtgata 4800  
Qy 8074 ctgctgatttaaccatggcgagcgtggagcggcggaataatagctgcacatcgtcgaa 8133  
Db 4801 ttgctttatttgtaacctataagctgcaataaaacaaagttaacaacaacattgcttc 4860  
Qy 8134 accagtgccccaggttcgggcaagggtcatccttggaagcgttaacttctccgcgcgat 8193  
Db 4861 attttatgttccaggttcagggggaggtgtgggaggttttttaagcaagtaaaacctct 4920  
Qy 8194 ctgcgcgtggactcgtgggtcctggccattctcatcgtgagctcgcggtgctcgcatat 8253  
Db 4921 acaaatgtggatggctgattgatcccggtcctgcgcgcttctcgtgtgagcgggta 4980





Db	2208	GCTCGGTTCCCAACGATCAAGCGCAGTTACATGATCCCCCATGTTGTCGCAAAAAGCGG	2149
QY	9862	ttagtccttcggtccctccatggtgtcagaagtaagttggtccgagtggttatcaactca	9921
Db	2148	TTAGCTCCTTCGGTCCCTCCGATCGTTGTCAGAAAGTAAGTTGGCCGAGGTGTTATCACATCA	2089
QY	9922	tggttatgagcagcactgataaattctctactgtcatcattccatccgtaagatgctttctg	9981
Db	2088	TGTTATGGCAGCACTGCATATTCCTTACTGTCTCATGCGCATCCGTAAAGATGCTTTTCGTG	2029
QY	9982	tgactggtgagtgactcaaccaagtcattctctgagaa tagtgtatggtggcgacgagtgctt	10041
Db	2028	TGACTGGTGTAGTACTCAACCAAGTCATTCGTGAGAATAGTGTATGCGCGCAGCGAGTGCT	1969
QY	10042	cttgcgcggtgcgaacggtgataataaccgcgcacatagcagaacttttaaagtgtcca	10101
Db	1968	CTTGCCCGCGCTCAATACGGGATTAATACCGCGCCACATAGCAGACTTTTAAAGTGTCTCA	1909
QY	10102	tcattggaacacgtcttcctggtggcgaaactctcaaggatcttaccgctgtgtgagatcca	10161
Db	1908	TCATTGGAACACGTTCTTCGGGGGAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCA	1849
QY	10162	gttcgatgaaccacactgtgcaccccaactgatcttcacgcatcttttactttccaccgctg	10221
Db	1848	GTTTCGATGAACCCACTCGTCACCACTGATCTTCAGCACTCTTTTACTTTCACCGGG	1789
QY	10222	ttctcgtgtgagcaaaacaggaaggcaaatgcgcgaacaaagggaataaaggcgacac	10281
Db	1788	TTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCCAAAAAGGAATTAAGGGCGACAC	1729
QY	10282	ggaatgttgaaactactctctctcttttcaatatattattgaagcattttatcagggtt	10341
Db	1728	GGAATGTGTAATCTCATACTCTCTCTTTTCAATATATTGAACATTTATCAGGGTT	1669
QY	10342	attgtctcatgagcggatcacatatttgaaatgtatttagaaaaataacaaatagggttc	10401
Db	1668	ATTGTCTCATGAGCGATACATATTGAAATGATATTTAGAAAAATAACAAATAGGGGTTTC	1609
QY	10402	cgcgcacatttccgcaaaagtgcacctgacgtcctaagaaccattattatcatgacat	10461
Db	1608	CGCGCACATTTCCCGAANAAGTGCACCTGACGCTTAAGNAACCATATTATCATGACAT	1549
QY	10462	taacctataaaataggcgtatcatcagggccctttcgtctcgcgcttccggtgatgacg	10521
Db	1548	TAACCTATAAAATAGGGGTATCATCAGAGGGCCCTTTCGTCTCGCGCGCTTCGGGTGATGACG	1489
QY	10522	gtgaaacactctgacacatgcagctcccgagacggtccacagcttctgtctgtaagcggatg	10581
Db	1488	GTGAAAACCTCTGACACATGACGCTCCCGGAGACGGTTCACAGCTTGTCTGTAAAGCGGATG	1429
QY	10582	ccgggagcagacaagcccgtcaggcgcgctcagcggggtgtgagggtgtcggggtggc	10641
Db	1428	CGGGAGCAGACAAGCCGTCAGGGCGCGTCAGCGGGGTGTGGCGGGGTCTCGGGGTGCG	1369
QY	10642	ttaactatcggcgcacagacagcagattgtactgagagtgaccatatgcggtgtgaaatac	10701
Db	1368	TTAACTATCGCGCATCAGACGAGATTGTACTGAGAGTGCACCATATATGCGGTGTGAAATAC	1309
QY	10702	cgcaccgaatcgcgcggaactaa	10724
Db	1308	CGCACAGATGCGTAAGGAGAAAA	1286
RESULT 6			
ABA04130/c			
ID	ABA04130 standard; DNA; 3755 BP.		
XX			
AC	ABA04130;		
XX			
DT	28-FEB-2002 (first entry)		
XX			
DE	Plasmid pHE19(II) polynucleotide sequence SEQ ID NO:4.		
XX			

KW	Promoter; gene expression; fermentation; D-AAT; Bacillus SK-1;
KW	D-amino acid aminotransferase; economic; large-scale protein production;
KW	circular; ds.
XX	
OS	Bacillus sp. SK-1.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..225
FT	/*tag= a
FT	/note= "specifically claimed promoter region in
FT	Claim 1 (see ABA04128)"
XX	
PN	WO200183787-A1.
XX	
PD	08-NOV-2001.
XX	
PF	26-APR-2001; 2001WO-JP03607.
XX	
PR	27-APR-2000; 2000JP-0128528.
XX	
PA	(BIOL-) BIOLEADERS CORP.
PA	(TAKI ) TAKARA SHUZO CO LTD.
XX	
PI	Sung M, Lee S, Hong S, Seo H;
XX	
DR	WPI; 2002-066535/09.
XX	
PT	Promoter sequence effective in Escherichia coli and Bacillus for
PT	economic large-scale fermentative production of proteins -
XX	
PS	Claim 7; Page 58-60; 65pp; Japanese.
XX	
CC	The present invention describes a DNA sequence (I) comprising promoter
CC	activity in Escherichia coli or Bacillus cells, where the promoter is
CC	derived from the D-AAT (D-amino acid aminotransferase) gene of
CC	Bacillus SK-1. (I) can be used for the high level expression of a
CC	foreign gene in a bacterial host for economic and efficient large-scale
CC	production of proteins such as enzymes, cytokines and antibodies. The
CC	present sequence represents the plasmid pHE19(II) polynucleotide
CC	sequence comprising a specifically claimed promoter region from the
CC	present invention.
XX	
SQ	Sequence 3755 BP; 951 A; 914 C; 932 G; 958 T; 0 other;
Query Match 18.2%; Score 2034.2; DB 24; Length 3755;	
Best Local Similarity 99.1%; Pred. No. 0;	
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;	
QY	8662 agttcaagaagaagcggtttttccataggtctccgccccctgacgagcatcaaaaaatc 8721
Db	3350 AGGCCCGCGTGTGCGCGTGTTCATAGGCTCCGCCGCCCTTGACGAGCATCACAAAAATC 3291
QY	8722 gacgctcaagtcagaggtggtgcgaacccgcagagactataaagataccagcggtttcccc 8781
Db	3290 GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGGTTCCCC 3231
QY	8782 ctggaagctccctcgtgcgctctcctgttcgcagccctgcgcgttacccggtacctgtccg 8841
Db	3230 CTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCGAGCCCTGCCGCTTACCGGATACCTGTCCG 3171
QY	8842 ctttctcccttcgggaagcggtggcgctttctcaatgctcacgctgtaggtatctcagtt 8901
Db	3170 CTTTCTCCCTTCGGGAAGCGGTGGCGCTTCTCAATGCTCAGCGTGTAGGTATCTCAGTT 3111
QY	8902 cgggtaggtcgttcgctccaaagctgggctgtgtgcagaaccccccggttcagccgacc 8961
Db	3110 CGGTGTAGGTCTCGTCCCTCAAGCTGGGCTGTGTGACGAACCCCGCTTCAGCCCGACC 3051
QY	8962 gctgcgcttatcccgtaactatcgtcttgatccaaacccggtgaagacagactatcgc 9021
Db	3050 GTTCGCCCTTATCCGGTAACATATCGTCTTGAGTCCAAACCCGGTAAGACAGACTTATCGC 2991

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QY 9022 cactggcagcaccactggttaacaggatttagcagagcaggtatgttagcggtgtacag 9081
DB 2990 CACTGGCAGCACCCTCGTAAACAGGATTAGCAGAGCAGGTATGTAGCGGTGTACAG 2931
QY 9082 agttctgaagtggtggcctaacctacgcgtacactagaagacagtatattggtatctcg 9141
DB 2930 AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGG 2871
QY 9142 ctctgctgaagccagttaccctctcgaaaaagagttggtagctcttgatcgcgcaacaaa 9201
DB 2870 CTCTGCTGAAGCCAGTTTACCTTCGGAAGAGAGTTGGTAGCTCTTGATCCGGCAACAAA 2811
QY 9202 ccacgcgtgttagcggtgtgttttctgttgcaagcagcagattacgcgcagaaaaaag 9261
DB 2810 CCACCGCTGGTAGCGGTGGTGTGTTTGTTCRAGCAGCAGATTACGCCGACAAAAAAG 2751
QY 9262 gatctcaagaaatcctttgatcttcttctacggggtctgcgctcagtggaacgaaact 9321
DB 2750 GATCTCAAGAAAGATCCTTTGATCTCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACT 2691
QY 9322 cactgttaagggatttggctcatgagattatacaaaaagagatcttcacctagatccttttaa 9381
DB 2690 CAGGTTAAGGGATTTTGGCTGATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTAA 2631
QY 9382 attaaaaatgaagttttaaatcaatctaaagtatatatagtaaaacttggtctgcagtt 9441
DB 2630 ATTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATATAGTAAACTTGGTCTGACAGTT 2571
QY 9442 accaatgcttaactagtgaggcaacctatctcagcgatctgtctattctgttcatccatag 9501
DB 2570 ACCAATGCTTAACTAGTGAGCAGCCTATCTCAGCGATCTGTCTATTTGCTTCATCCATAG 2511
QY 9502 ttgctctgactccccctcgttagataactacgatacggagaggtctaccatctgcccaca 9561
DB 2510 TTGGCTGACTCCCTCGTGTAGATTAATCTACGATACGGGAGGCTTACCATCTGGCCCCA 2451
QY 9562 gtgtgtcaatgatgaccgagaccacgcgtcaccgggtccagatttatcatcagcaataaacc 9621
DB 2450 GTGCTGCAATGATACCGCGAGACCACGCTCACCGGCTCCAGATTTTATCAGCAATAAACC 2391
QY 9622 agcagcgggaagggccgcgagcgaagtggttctcgaactttatccgctccatccagt 9681
DB 2390 AGCCAGCGGAGGCGCCGCGCAGAGTGGTCTCGCACTTTATCCGGCTCCATCCAGT 2331
QY 9682 ctattaattgttgcgggaagctagatgaagtagttgcagttaatagtttgcgcaacg 9741
DB 2330 CTATTAAATGTTGCGGGAAAGCTAGAGTAAGTAGTTGCGCCAGTTAATAGTTTGGCAACG 2271
QY 9742 ttgttgccattgtcacaggtcgtgtgtcgcgctcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 9801
DB 2270 TTGTTGCCATTGCTACAGSCATCGTGGTGTACAGCTCGTGTGTGTGTGTGTGTGTGTGT 2211
QY 9802 gtcctgggttcccaacgatacaggcgagttacatgatcccccatgttgtgtgcataaagcgg 9861
DB 2210 GCTCGGGTTCCCAACGATCAAGGCGAGTTACATGATCCGCCCATGTTGTGCAAAAAAGCGG 2151
QY 9862 ttagctccctcgtgctcctcgtatgtgtcagaagtaagttggccgcagtggttatcatcaca 9921
DB 2150 TTAGTCTCTTCGGTCTCCGATCGTGTGCAGAAGTAAGTTGGCCGCGAGTGTATCACTCA 2091
QY 9922 tgggtatggcagcaactgataaattctcttactgtcatgcatacgcgaagatctttctgt 9981
DB 2090 TGGTTATGGCAGCACTGATAAATTTCTTACTGTCTATGTCATCCGTAAGATGCTTTTCTG 2031
QY 9982 tgactgggtgagtactcaaccagtcattctgagaatagtgatgtgcggcgaccgagttgct 10041
DB 2030 TGACTGGTGTAGTACTCAACCAAGTCAATCTGAGAATAGTGTATGCGGCGACCGAGTTGCT 1971
QY 10042 cttgcggcggtcacaacgagataaataccgcgcacatacagacaactttaaagtgctca 10101
DB 1970 CTTGCCGCGCTCAATACGGGATTAATACCGCGCCACATAGCAGAACTTTTAAAGTGCTCA 1911
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QY 10102 tcattggaaaaacgttcttcctgggggcgaaaaactcacaaggatcttaccgctgttgagatcca 10161
DB 1910 TCATTGGAAAAACGTTCTTCGGGGCGGAAAACTCTCAAGGATCTTTACCGCTGTGTGAGATCCA 1851
QY 10162 gttcgtatgtaaacccactcgtcaccccaactgattctcagcatcttcttactttccaccagcg 10221
DB 1850 GTTCGATGTAAACCCACTCGTGTCACCCAACTGATCTTCAGCATCTTTTACTTTTACCACAGG 1791
QY 10222 ttctcgggtgagcaaaaaacaggaaggcaaaatgccgcacaaaaagggaaataagggcgacac 10281
DB 1790 TTCTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACAC 1731
QY 10282 gaaaatgttgtaactcactactcttcttcttcaatatatttgaagcattttatcagggtt 10341
DB 1730 GGAATGTTGAATACTCATCTCTTCTCTTCAATATATTATGAAGCATTTATCAGGGTT 1671
QY 10342 attgtctcatgagcgggatacatatttgaatgtattttagaaaaataaaaaataggggttc 10401
DB 1670 ATTGTCTCATGAGCGGATACATATTTTGAATGTATTTTAGAAAAATAAACAAATAGGGGTTTC 1611
QY 10402 cgcgcacatttcccgcgaaaagtgcacctgacctgacctgacctgacctgacctgacctgacct 10461
DB 1610 CGCGCACATTTCCCGCGAAAAAGTGCCACCTGACGCTCTAAGAAAAACCATTTATCATGACAT 1551
QY 10462 taacctataaaaaataggcgatatcacaggcccttctcgtcgcggtttcgttgatgacg 10521
DB 1550 TAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCTGTCTCGCGCGTTTCGGTGTATGAGC 1491
QY 10522 gtgaaaaacctctgacacatgcagctcccgcgagcgtcacagcttctgttgaagcggatg 10581
DB 1490 GTGAAAACTCTGTACACATGCAGCTCCCGAGAGCGGTCTACAGCTTGTCTGTAAAGCGGATG 1431
QY 10582 ccggagcagacaagcccgctcagggcgctcagcggtgtcagcggtgttgcggtgtcgggctggc 10641
DB 1430 CCGGAGCAGCAGACGCCGCTCAGGGCGGCTCAGGGGCTGTGCGGGGTCTCGGGGCTGGC 1371
QY 10642 ttaactatgcggcatcagcagcagatttactagagatgcacatatgcggtgtgaaatac 10701
DB 1370 TTAACATATGCGGCATTCAGAGCAGATTGTACTGAGATGTCACCATATGCGGTGTGAAATAC 1311
QY 10702 cgcaccgaatcgcgcggaactaa 10724
DB 1310 CGCACAGATGCGTAAGGAGAAAA 1288
RESULT 7
AAV12067/c
ID AAV12067 standard; cdna; 4713 bp.
XX
AC AAV12067;
XX
DT 08-JUN-1998 (first entry)
XX
DE Murine IAD alpha chain cDNA.
XX
KW Major histocompatibility class II antigen; MHC class II; T cell;
KW T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell;
KW APC; autoimmune disease; diabetes; diabetes; multiple sclerosis;
KW autoimmune thyroiditis; systemic lupus erythematosus;
KW myasthenia gravis; Crohn's disease; inflammatory bowel disease;
KW allergy; asthma; contact sensitivity; immunotherapy; therapy;
KW IAD alpha chain; mouse; ds; circular; cyclic.
XX
OS Mus musculus.
XX
PN WO9746256-A1.
XX
PD 11-DEC-1997.
XX
PF 22-MAY-1997; 97WO-US08697.
XX
PP 23-MAY-1996; 96US-0018175.
XX
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Db	2760	TTTTCTGGGTGACAAAAACAGGAAGGCAAAATCCGCAAAAGGAATTAAGGGCGACAC	2701
QY	10282	ggaaatgttgaatactcatactcttccttttccaattatttgaagcatttatcagggtt	10341
Db	2700	GGAATAATGTTGAATACTCATACTCTTCCTTTTCAATATATTGAAGCATTTATCAGGCTT	2641
QY	10342	attgtctcatgacgcgatcacatatattgaattgtattttagaataatacaaatagggttc	10401
Db	2640	ATTGTCTCAAGCGGATACATATTTGAATGATTTAGAAAATAAACAATATGGGGTTC	2581
QY	10402	cgcgcacattcccgcgaaaagtgcacactgacgtctaagaacattattatcatgacat	10461
Db	2580	CGCGCACATTTCCCGGAAAAGTGCACTGACGCTGAAGAACCATTTATCATGACAT	2521
QY	10462	taacctataaaaatagcgatcacgagggcccttcgtctccgcggtttcgttgatgacg	10521
Db	2520	TAACTTATAAAATAGCGGTATACGAGGGCCCTTTCGTCTCGCGGTTTCGGTGATGACG	2461
QY	10522	gtaaaacctcttgacacatgcagctcccgagagcgggtcacagcttgtctgtaagcggatg	10581
Db	2460	GTGAAAACCTCTGACACATGCAGCTCCGAGAGCGGTCAAGCTGTCTGTGAAGCGGATG	2401
QY	10582	ccgggagcagacaagcccgctcaggcgcgctcagcgggtgttgacgagtgtcggggctggc	10641
Db	2400	CCGGGAGCAGACAAACCCGTGAGGGCGCTCAGCGGGTGTGGCGGGTTCGGGGCTGGC	2341
QY	10642	tbaactatgcgcacatcagacagagatttactagagtgcacatatgcggtgtgaaatac	10701
Db	2340	TTAACTATCGCGCNTCAGACAGAGATTGTACTGAGAGTGCACCATATGCGCGTGTGAAATAC	2281
QY	10702	cgcaccggaatcgcgcggaaataa	10724
Db	2280	CGCACAGATCGCGTAAGAGAGAAAA	2258

RESULT	8	
ID	AAV12068/C	
AD	AAV12068 standard; cDNA; 4724 BP.	
XX		
XX	AAV12068;	
AC		
XX		
XX	08-JUN-1998 (first entry)	
DT		
XX		
XX	Murine IAD beta chain cDNA.	
DE		
XX		
KW	Major histocompatibility class II antigen; MHC class II; T cell;	
KW	T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell;	
KW	APC; autoimmune disease; diabetes; multiple sclerosis;	
KW	autoimmune thyroiditis; systemic lupus erythematosus;	
KW	myoschlenia gravis; Crohn's disease; inflammatory bowel disease;	
KW	allergy; asthma; contact sensitivity; immunotherapy; therapy;	
KW	IAD beta chain; mouse; ds; circular; cyclic.	

allergy, e.g. asthma and contact sensitivity

Example 2; Page 94-96; 141pp; English.

This nucleotide sequence comprises a PCR product obtained by amplification of mouse splenocyte cDNA using primers (see AA12065 and AA12066) designed for the amplification of IAD beta chain full-length cDNA. IAD alpha chain cDNA (see AA12067) has been similarly obtained. The IAD sequences were cloned into metallothionein promoter (see AA12062)-driven vector pRmH-3 prior to sequencing. Major histocompatibility complex (MHC) class II IAD heterodimers were expressed at the cell surface of transfected *Drosophila* Schneider 2 (ATCC CRL 10974) cells. The invention relates to the preparation and use of synthetic antigen presenting matrices, in particular antigen presenting cells such as insect cells that have been transfected to produce MHC antigen presenting molecules with one or more accessory molecules. The matrices are used to activate naive CD4<sup>+</sup> T cells and to shift the ongoing activation state into a preferred differentiated population of Th1 or Th2 cells. Applications include the treatment of autoimmune disease, e.g. diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel disease, or an allergy, e.g. asthma and contact sensitivity.

Sequence 4724 BP: 1196 A; 1194 C 1200 G; 1134 T; 0 other;

Query Match									
Best Local Similarity		18.2%		Score 2034.2		DB 19		Length 4724	
Matches 2045		Conservative		Pred. No. 0		Mismatches		18	
								Indels 0	
Qy	8662	agttcaagaagaagcgctttttccatagtgctccgccccctgacgagcatcacaaaaac	8721						
Db	4331	AGGCCGCGTtGCTGGCGTtTTTTCATAGStCTCCGCCCCCTGACGAGCATCACAAAATC	4272						
Qy	8722	gacgtcaagftcaagdtgacagcgcgaacccagagacatataaatacacaggcgtttccc	8781						
Db	4271	GACGCTCAAGTTCAGAGTGGCGAAACCCAGAGACATATAAGATACCAGGCGTtTCCCC	4212						
Qy	8782	ctggaagctccctcgctgcgtctctctgtttccgaacctgcgcgttacccgataccctgtccg	8841						
Db	4211	CTGGAAAGTCCTCTCGTCGCTCTCTCTGTTCGACCCCTGCCGCTTACGGATACCTGTCCG	4152						
Qy	8842	cccttcccttcgggaagcgtgagcgtcttctcaatgctcacgctcaggtatctcagtt	8901						
Db	4151	CCTTCTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCASTT	4092						
Qy	8902	cggtagtgcttgcgtccaaagtgggctgtgtgcagcaaccccccttcagcccgacc	8961						
Db	4091	CGGTGTAGTGTGCTTCACAGCTGGGTGTGTGTGCAGAACCCCGCTTASCCCGACC	4032						
Qy	8962	gctgcgccttatccggtaaactatcgtcttgagtccaacccggtaaagacagacttatcgc	9021						
Db	4031	GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCACCCGGTAAGACACGACTTATCGC	3972						
Qy	9022	cactggcagagcaactggttaaaggattagcagagcaggtatgtaggcgtgtctaacag	9081						
Db	3971	CACtGGCAGCAGCCACCTGGTAACAGGATTTAGCAGGCGAGGTATGTAGCGGTGTCTACAG	3912						
Qy	9082	agttctgaadtgtggccttaactacgctacactagaaggacagttatttggtatctcgcg	9141						
Db	3911	AGTtCTTGAAGTGTGGCCCTAACTACGGCTACACTAGAAAGCAGATATTGTGTATCTCGC	3852						
Qy	9142	ctctctgaagccagtttaaccttcggaaaaaagttgtagctcttgatccgcgcaacacaa	9201						
Db	3851	CtCTGCTGAAGCCAGTAACTTCGGAAAAAGATTGGTGTACTCTTGATCCGCAACACAA	3792						
Qy	9202	ccaccgctggtagcggtyggttttttggtttgcagcagcagatatcgcgcagaaaaaag	9261						
Db	3791	CCACCgCTGTGTAGCGGTGGTTTTTTTGTGTGCAGACAGATTACGCACGCAAAAAAG	3732						
Qy	9262	gatctcaagaagaacctttgatctttcttaoqgggtctgcacgtccagttggacgcgaaact	9321						

|||||  
Db 3731 GATCTCAAGAAGATCCTTTGATCTTTTACGGGCTCTGACGCTCAGTGGAAACGAAACT 3672  
Qy 9322 caggttaaggagatttgggtcagtagattatcaaaaaaggagattctcaactagatcccttttaa 9381  
Db 3671 CAGGTTAAGGGATTTGGTGCATCAGAGATTATCAAAAAAGGATCTTCACCTAGATCCTTTTAA 3612  
Qy 9382 attaaaaatgaagtttttaaatcaacttaaaagtatatatagtaaacttggctgcaggtt 9441  
Db 3611 ATTTAAAAATGAAGTTTAAATCAATCAATCAAGTATATATGAGTAAACTTGCTGTGACAGTT 3552  
Qy 9442 accaatgcttaatoagtgaggacacttatctcagcagatctgtctatttctgttcaatcag 9501  
Db 3551 ACCAATGCTTAAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCGTTTCATCCATAG 3492  
Qy 9502 ttgcctgaactcccgctgtatgaataactacgatacggagggtcttaccatctggcccca 9561  
Db 3491 TTGCCTGACTCCCGCTGTGTAGTAACTACGATACGGGAGGGCTTACCATCTGGCCCCA 3432  
Qy 9562 gtgctgcaatgataccgcgagacccacgcgtcacccggtccagattttatcagcaataaacc 9621  
Db 3431 GTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACC 3372  
Qy 9622 agccagccggaaggccgagcgagagaagtggctcctgcaactttatccgctccatccagt 9681  
Db 3371 AGCCAGCGGAAGGCGGAGCGCAGAGAGTGGTCTGCAACTTTATCCGCCCTCCATCCAGT 3312  
Qy 9682 ctattaattgttcgcggaagctagatgaagttagttcgcaggttaataagtttgcgaacg 9741  
Db 3311 CTATTAATGTTCGGGGAAGCTAGATGAAGTAGTGTGCCAGTTAATAGTTTGGCAACG 3252  
Qy 9742 ttgttgcaattgctacaggcatcgtggtgtcacgctcgtcgttgggtatggcttcattca 9801  
Db 3251 TTGTTGCCATTGCTACAGGCATCTGTGTGTACGCTCGTCTGTTGGTATGGCTTCATTCA 3192  
Qy 9802 gctccggttcccaacgatcaaggcaggttacatgatacccccatgttgtcaaaaaagcgg 9861  
Db 3191 GCTCGGTTCCCAAGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG 3132  
Qy 9862 ttagtccttcggctccgctcgcgtgtgtcagaagtaagttggccgcagtggttatcaatca 9921  
Db 3131 TTAGTCTCTCCGTTCCGATCGTTGTGCAGAAAGTAAGTTGGCCGCAGTGTATCACTCA 3072  
Qy 9922 tggttatggcagactgataattctcttactgtcatgccaatccgtaagatgctttctg 9981  
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ID AAX77617 standard; DNA; 4776 BP.  
XX  
AC AAX77617;  
XX  
DT 13-AUG-1999 (first entry)  
XX  
DE Expression construct pTC53 DNA.  
XX  
KW Pseudo-type retroviral vector; surface capsid protein; virus core;  
KW retroviral packaging cell; psi-negative expression construct; gag gene;  
KW pol gene; cell-specific transduction; cell targeting; gene therapy;  
KW vaccination; diagnosis; cystic fibrosis; ADA-deficiency; HIV-1 infection;  
KW chronic granulomatosis; ss.  
XX  
OS Spleen necrosis virus.  
OS Mus sp.  
OS Synthetic.  
XX  
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DT	13-AUG-1999 (first entry)		
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KW	Cell-specific retroviral vector; antibody domain; vaccination; scFv;		
KW	cell-specific transduction; B cell RNA; variable region; heavy chain;		
KW	light chain; immunoglobulin; psi-negative; retroviral Env protein;		
KW	capsid protein; cell targeting; gene therapy; diagnosis; cystic fibrosis;		
KW	ADA-deficiency; chronic granulomatosis; HIV-1 infection; ds.		
XX			
OS	Spleen necrosis virus.		
OS	Mus sp.		
OS	Synthetic.		
XX			
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FT FT /note= "CDS 29"

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WO9928489-A2.

10-JUN-1999.

XX

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PF 27-NOV-1998; 98WO-DE03543.
XX
PR 28-NOV-1997; 97DE-1052854.
XX
PA (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI Cichutek K, Engelstaedter M;
XX
DR WPI; 1999-371131/31.
XX
XX
XX Cell-specific retroviral vectors with antibody domains suitable for
XX cell-specific transduction of selected mammal cell types - useful
XX for vaccination and gene therapy for treatment of, e.g. cystic
XX fibrosis
XX
XX Disclosure; Fig 4A-B; 38pp; German.
XX
XX This invention describes the construction of novel cell-specific
XX retroviral vectors with antibody domains suitable for cell-specific
XX transduction of selected mammal cell types. The invention describes a
XX method to produce cell-specific retroviral vectors which consists
XX essentially of the following steps: (a) immunization of a mammal with
XX one or more cell populations (b) isolation of RNA from the immunized
XX mammal, especially the B cell RNA (c) production of a cDNA strand of
XX the variable region of the heavy and light chains of the immunoglobulins
XX isolated from the RNA by RT-PCR with primers for the respective
XX immunoglobulin chains, where the primer nucleic acid sequences are for
XX an oligopeptide linker (d) ligation of the cDNA strain to scFv-cDNA (e)
XX ligation of the scFv cDNA in a phagemid vector and transformation of a
XX host bacterium with the vector (f) isolation of phage, by selection of
XX phage that bind to the cell population used in step (a) (g) cleavage of
XX the scFv coding DNA fragments from the cell-specific phage and ligation
XX into a psi-negative retroviral Env-expression vector (h) transfection
XX of a Env-ScFv expression vector to be maintained in a packaging cell and
XX (i) isolation of a packaging cell with the retroviral vectors. The
XX pseudo-type retroviral vectors with modified surface capsid proteins are
XX suitable for cell-specific transduction of a selected mammal cell type
XX (cell targeting). The methods are useful for the production of the
XX pseudo-type retroviral vectors and for gene transfer in selected cell
XX types. The vectors can be used in medicaments for gene therapy,
XX vaccination or diagnosis. They are particularly useful for therapy of
XX cystic fibrosis, ADA-deficiency, chronic granulomatosis or HIV-1
XX infection. This sequence represents the expression construct pTC53
XX which is composed from the SNV Env protein and a murine derived scFv
XX fragment. This sequence encodes the protein fragments represented in
XX AAY08761-Y08790.
XX
XX Sequence 4776 BP; 1199 A; 1178 C; 1245 G; 1154 T; 0 other;
XX

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Query Match 18.2%; Score 2034.2; DB 20; Length 4776;
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Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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AC AAT13390;  
XX  
DT 24-JUN-1996 (first entry)  
XX  
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XX  
KW Hybrid; vector; gene transfer; gene therapy; haematopoietic stem cell;  
KW retroviral; murine embryonic stem cell virus; MESV;  
KW Moloney murine sarcoma virus; (MoMuSV);  
KW Friend murine leukaemia virus; F-MuLV; ds.  
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OS Synthetic.  
XX  
PN DE19503952-A1.  
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PD 14-MAR-1996.  
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PF 07-FEB-1995; 95DE-1003952.  
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AC AAT13393;  
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DT 24-JUN-1996 (first entry)  
DE Hybrid vector pMM1.  
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KW Hybrid; vector; gene transfer; gene therapy; haematopoietic stem cell;  
KW retroviral; murine embryonic stem cell virus; MESV;  
KW Moloney murine sarcoma virus; (MoMuSV);  
KW Friend murine leukaemia virus; F-MuLV; ds.  
OS Synthetic.  
SS  
PN DE19503952-A1.  
XX  
PD 14-MAR-1996.  
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PR 08-SEP-1994; 94DE-1431973.  
XX  
PA (BOE ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Baum C, Ostertag W, Stocking-harbers C, Stockingharbers C;  
XX  
DR WPI; 1996-152306/16.  
XX  
PT Hybrid retroviral vectors - for gene transfer into haematopoietic  
PT stem cells  
XX  
PS Claim 10; Page 21-25; 42pp; German.  
XX  
CC New hybrid vectors comprise (1) a leader region including the U5  
CC region and TRNA primer binding site of murine embryonic stem cell  
CC virus (MESV) or Moloney murine sarcoma virus (MoMuSV), and (2) a 3'-  
CC LTR including the U3 and R regions of a Friend murine leukaemia  
CC virus (F-MuLV). The vectors are useful for ex-vivo or in-vivo gene  
CC therapy. High levels of gene transfer can be achieved in  
CC haematopoietic stem cells and their myeloid (non-lymphatic) progeny.  
CC pSF1, pSF2, pSF3 and pMM1 (sequences given in AAT13390-R13393) are  
CC examples of such vectors.  
CC Vector pSF-MDR (sequence given in AAT13394) is based on the  
CC MESV vector R224.

XX  
SQ Sequence 5364 BP; 1233 A; 1454 C; 1355 G; 1322 T; 0 other;  
  
Query Match 18.2%; Score 2034.2; DB 17; Length 5364;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 8662 agttcaagaagaaggcggtttttccataggtccgcggcccccctgacgagcatcacaaaaatc 8721  
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Db 3290 aggcgcggttgcgtggtttttccataggtccgcggcccccctgacgagcatcacaaaaatc 3349  
QY 8722 gacgctcaagtacagagtggtgcgaaccccgacagagactaaagataccacgagcgtttcccc 8781  
|||  
Db 3350 gacgctcaagtacagagtggtgcgaaccccgacagagactaaagataccacgagcgtttcccc 3409  
QY 8782 ctggaagctccctcgtgcgctctctctgttcgaacccctgcgcttacccgataccctgtccg 8841  
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Db 3410 ctggaagctccctcgtgcgctctctctgttcgaacccctgcgcttacccgataccctgtccg 3469  
QY 8842 cctttctcccttcgggaagcgtggcgcttctcaatgctcacgctgtaggtatctcagtt 8901  
|||||  
Db 3470 cctttctcccttcgggaagcgtggcgcttctcaatgctcacgctgtaggtatctcagtt 3529  
QY 8902 cgtgtaggtcgttcgctccaaagctgggctgtgtgcagaaacccccccttcagcccagcc 8961  
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Db 3530 cgtgtaggtcgttcgctccaaagctgggctgtgtgcagaaacccccccttcagcccagcc 3589  
QY 8962 gctgcgccttatccggttaactatcgtcttgagtcacaccccggtgaagcacgacttatcgc 9021  
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Db 3590 gctgcgccttatccggttaactatcgtcttgagtcacaccccggtgaagcacgacttatcgc 3649  
QY 9022 caetggcagcagccactggttaacagagattagcagagcaggtatgtagggcgtgctacag 9081  
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Db 3650 caetggcagcagccactggttaacagagattagcagagcaggtatgtagggcgtgctacag 3709  
QY 9082 agttctgaagtggtgcgttaactacgctacacactagaagacagatattgtatctcgcg 9141  
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QY 9142 ctctgtgaaggcagttacctctcggaagagtggtgtagctctctgtatcccggaacacaa 9201  
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Db 3770 ctctgtgaaggcagttacctctcggaagagtggtgtagctctctgtatcccggaacacaa 3829  
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Db 3890 gatcacaagaagatcccttgatcttttctacggggtctgcagcgtcagtggaacgaaact 3949  
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Db 4190 gtgctgaatgataccgcgagaccccgctccaccgggtccagatttatcagcaataaac 4249  
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Db 4250 agccagccggaagggccgagcgagagtggtcccgcaactttatccgcctccatccagt 4309
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Db 4310 ctataattgttccg99aagctagagtaagttagtctgccagtttaataagtttgcgaacg 4369
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Qy 10222 tttctggtgagcaaaaaacggaagcaaaaatgccgcgcaaaaaaggaataaggcgcgacac 10281
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Db 5270 ttaactatcgggcatcagagcagattgttactgagagtgaccacatatcggtgtgtaataac 5329
Qy 10702 cgcaccgaatcgcgcggaactaa 10724
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Db 5330 cgcacagatgcgtaaggagaaaa 5352

RESULT 13
AAC60706
ID AAC60706 standard; DNA; 5374 BP.
XX
AC AAC60706;
XX
DT 30-JAN-2001 (first entry)
XX
DE Primers attached vector elongation method vector pED6pdc2.
XX
KW Primers attached vector elongation; PAVE; plasmid vector;
cDNA library construction; ds.
XX
OS Synthetic.
XX
PN WO200056913-A1.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07332.
XX
PR 19-MAR-1999; 99US-0125596.
XX
PA (GEMY ) GENETICS INST INC.
XX
PI Song C, Brown JC, Leeying W, Rivera DS;
XX
XX WPI; 2000-638266/61.
XX
PT Preparing modified a mRNA molecule for constructing a cDNA library
comprises ligating a tag which consists of ribonucleotide residues and
does not have any deoxyribonucleotide residues, to the 5' end of an
mRNA molecule -
XX
XX Disclosure; Fig 6; 65pp; English.
XX
The present invention is concerned with a novel method for cDNA library
construction. This involves the use of tagged sample mRNA molecules for
amplification using primers contained within vectors. The RNA is then
digested, second strand synthesis is performed and the resulting molecule
comprises a vector containing the desired cDNA sequence. The present
sequence is a vector used to demonstrate the method. The method can be
used as a more efficient and reliable way of obtaining full-length cDNA
libraries. The method is known as primers attached vector
elongation (PAVE).
XX
SQ Sequence 5374 BP; 1320 A; 1337 C; 1399 G; 1318 T; 0 other;
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Query Match 18.2%; Score 2034.2; DB 21; Length 5374;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 3138 aggcgcgctgtgcgctttttccataggtcgcgcctcagcagatcacaaaaatc 3197

Qy 8722 gacgtcaagtacagagtggtggaacccgacaggactataaagataccaggcgtttcccc 8781
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Db 3198 gacgtcaagtacagagtggtggaacccgacaggactataaagataccaggcgtttcccc 3257

Qy 8782 ctgaaagctccctcgtcgtctcctcgttcgcacctcgccttaccgataacctgtccg 8841
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Db 3258 ctgaaagctccctcgtcgtctcctcgttcgcacctcgccttaccgataacctgtccg 3317

Qy 8842 cctttctcccttcgggaagcgtggtcgtcttctcaatgtcagcgtgtagggtatctcagtt 8901
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Db 3318 cctttctcccttcgggaagcgtggtcgtcttctcaatgtcagcgtgtagggtatctcagtt 3377

Qy 8902 cgggtgtaggttcgttcgtctccaagctgggctgtgtgcagcaaccccccggttcagcccgacc 8961
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Db 3378 cgggtgaggtcgtccgaagctgggctgctgcgaaccccccgcttcagcccgacc 3437  
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Qy 10582 ccgagagacaacaccccgtaacggcgctcagcggtgttcgcggtgttcgagggctgcgc 10641  
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Db 5118 ttaactatgagcgcacatgagcagattgtactgagagtgacaccatgctggttgaaatac 10701  
Qy 10702 cgcacccaatcgcggaactaa 10724  
Db 5178 cgcacagatgcgtaaggagaaaa 5200  
RESULT 14  
AAC68299 standard; DNA: 5421 BP.  
XX AC AAC68299;  
XX XX AC  
DT 20-FEB-2001 (first entry)  
XX SV40/APPA plasmid coding sequence.  
DE Transgenic animal; salivary protein; phytase; phosphorus; animal growth;  
XX environmental pollution; pig; ds.  
KW Rhesus macaque polyoma virus - chimeric.  
XX Escherichia coli - chimeric.  
OS WO200064247-A1.  
PN 02-NOV-2000.  
XX 20-APR-2000; 2000WO-CA00430.  
PF XX

PR 23-APR-1999; 99US-0130508.  
 XX (UYGU-) UNIV GUELPH.  
 XX  
 XX Forsberg CW, Golovan S, Phillips JP;  
 XX  
 XX WPI; 2000-687245/67.  
 DR P-PSDB; AAB36262.  
 DR  
 XX Transgenic non-human animal for gastrointestinal tract specific  
 PT expression of a protein, preferably phytase, comprises a nucleic acid  
 PT sequence including a heterologous transgene construct encoding the  
 PT protein -  
 XX  
 XX Claim 56; Fig 22; 152pp; English.  
 PS  
 XX The present invention provides transgenic animals which produce desired  
 CC proteins, in this case pigs which expresses phytase in the salivary  
 CC gland. Low phytase production levels result in phytate in the diet being  
 CC excreted and causing phosphorus contamination in water, as well as  
 CC reducing the growth of animals. The invention provides a number of  
 CC transgenes containing the E. coli APPA phytase coding sequence.  
 XX  
 SQ Sequence 5421 BP; 1413 A; 1321 C; 1331 G; 1355 T; 1 other;

Query Match 18.2%; Score 2034.2; DB 21; Length 5421;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps

QY	8662	agttcaagaagaaggcggtttttccataggtccgcgccccctgacgagcatcacaaaaac	8721
DB	2687	agggcggtgtcggggtttttccataggtccgcgccccctgacgagcatcacaaaaac	2746
QY	8722	gacgctcaagtcagaagtgcgcaaacccacagagactataaagataccaggcgtttcccc	8781
DB	2747	gacgctcaagtcagaagtgcgcaaacccacagagactataaagataccaggcgtttcccc	2806
QY	8782	ctggaagctccctcgtcgctctccctgttccgacctgcgcttacccgataccctgtccg	8841
DB	2807	ctggaagctccctcgtcgctctccctgttccgacctgcgcttacccgataccctgtccg	2866
QY	8842	ctttctccctcgggaagcgtggcgcttctccaatgtccacgctgtaggtatctcagtt	8901
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QY	8902	cggtgtagtgcgttcgctccaaagctggcgtgtgtgcagaaacccccctcagcccgacc	8961
DB	2927	cggtgtagtgcgttcgctccaaagctggcgtgtgtgcagaaacccccctcagcccgacc	2986
QY	8962	gctgcgcttatccggttaactatcgctttgagtcacacccggttaagacacgacttatcgc	9021
DB	2987	gctgcgcttatccggttaactatcgctttgagtcacacccggttaagacacgacttatcgc	3046
QY	9022	cactgcagcagccactgataacagattagcagacgaggtatgtagcggtgctacag	9081
DB	3047	cactgcagcagccactgataacagattagcagacgaggtatgtagcggtgctacag	3106
QY	9082	agttcttgaagtgtgtggcctaaactacgctacactagaaagacagattttggtatctcgc	9141
DB	3107	agttcttgaagtgtgtggcctaaactacgctacactagaaagacagattttggtatctcgc	3166
QY	9142	ctctcgtgaagccagtttaacttcgaaaaaagattggtagctcttgatcccggaacaaa	9201
DB	3167	ctctcgtgaagccagtttaacttcgaaaaaagattggtagctcttgatcccggaacaaa	3226
QY	9202	ccaccgctggtgagcgtggtttttttgttgcagacgacagattacgcgcagaaaaaag	9261
DB	3227	ccaccgctggtgagcgtggtttttttgttgcagacgacagattacgcgcagaaaaaag	3286
QY	9262	gattccaagaagatactctttgatctttttctacggggtctgcgcgtcagtcggaacaaact	9321
DB	3287	gattccaagaagatactctttgatctttttctacggggtctgcgcgtcagtcggaacaaact	3346



Search completed: September 21, 2002, 08:03:09  
Job time: 33118 sec

Qy 9682 ctattaatgttgccgggaagctagagtaagtagttccgcaagttaatagtttgcgcaagc 9741  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 22:09:21 ; Search time 19406.3 Seconds  
(without alignments)  
12083.829 Million cell updates/sec

Title: US-09-700-843-1  
Perfect score: 11206  
Sequence: 1 catgatgaataacataagg.....cacgatgagaatggccagac 11206

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
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9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vi:*
30: em.htg_hum:*
31: em.htg_inv:*
32: em.htg_other:*
33: em.htgo_inv:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

	1	11206	100.0	11206	6	E30143	E30143 Vector for
	2	11195	99.9	11207	3	AB028139	AB028139 Drosophila
	3	5433.2	48.5	8780	12	PEU59056	US9056 P element t
	4	5433.2	48.5	9255	12	PEU60735	U60735 P element t
c	5	5096.2	45.5	12294	12	DMCASP2C2	X11643 D.melanog
	6	5055.4	45.1	10020	12	AF242362	AF242362 Green Pel
	7	5055.4	45.1	10095	12	AF242364	AF242364 Stinger Pel
	8	5055.4	45.1	10189	12	AF242363	AF242363 Green H-P
	9	5055.4	45.1	10288	12	AF242365	AF242365 H-Stinger
	10	5055.4	45.1	13336	12	AF242360	AF242360 Pelican 1
	11	5055.4	45.1	13508	12	AF242361	AF242361 H-Pelican
	12	5044	45.0	7862	12	DMCASP4	X11645 D.melanog
	13	5042.6	45.0	7815	12	PEU59054	US9054 P element t
	14	5042	45.0	7775	12	DMCASP1	X11644 D.melanog
	15	5041.6	45.0	7815	12	PEU59055	US9055 P element t
c	16	2891.8	25.8	3271	8	SCYPL248C	Z73604 S.cerevisia
	17	2891.8	25.8	3694	8	YSGAL4	K01486 Yeast (S.ce
	18	2891.8	25.8	37808	8	SC38KCVI	Z67751 S.cerevisia
c	19	2760	24.6	3616	12	SYNNEGIE	M30841 Vector cont
	20	2628.4	23.5	2646	6	E06922	E06922 DNA encodin
	21	2538.2	22.7	14245	3	DMWHITE	X02974 Drosophila
	22	2439.6	21.8	7485	2	AC013055	AC013055 Drosophila
c	23	2439.6	21.8	45752	3	DMN33B1	AL133506 Drosophila
	24	2439.6	21.8	162436	2	AC104145	AC104145 Drosophila
c	25	2439.6	21.8	300205	3	AE003425	AE003425 Drosophila
	26	2143.2	19.1	8932	12	U03463	U03463 Cloning vec
	27	2108.8	18.8	5805	3	DSU64875	U64875 Drosophila
	28	2103	18.8	9386	12	U03462	U03462 Cloning vec
	29	2102.8	18.8	7286	6	AR112486	AR112486 Sequence
c	30	2102.8	18.8	7286	6	E34421	E34421 Inductive p
	31	2034.2	18.2	2905	12	SYNPKP497A	M74187 Cloning vec
c	32	2034.2	18.2	3024	1	PK9CDB	L27082 plasmid KIL
	33	2034.2	18.2	3024	12	SYNCCDBC	L38497 Cloning vec
c	34	2034.2	18.2	3582	12	SYNCCOMCS	M68946 Cloning vec
	35	2034.2	18.2	3642	12	SYN260BLA	M29362 Plasmid pFL
c	36	2034.2	18.2	3875	6	AR147724	AR147724 Sequence
	37	2034.2	18.2	3875	6	AR159746	AR159746 Sequence
c	38	2034.2	18.2	3875	6	AR160438	AR160438 Sequence
	39	2034.2	18.2	3878	6	AR147730	AR147730 Sequence
c	40	2034.2	18.2	3878	6	AR159752	AR159752 Sequence
	41	2034.2	18.2	3878	6	AR160444	AR160444 Sequence
c	42	2034.2	18.2	3883	6	AR147733	AR147733 Sequence
	43	2034.2	18.2	3883	6	AR159755	AR159755 Sequence
c	44	2034.2	18.2	3883	6	AR160447	AR160447 Sequence
	45	2034.2	18.2	3908	6	AR147727	AR147727 Sequence

#### ALIGNMENTS

RESULT	1	E30143	11206 bp	DNA	linear	PAT 07-FEB-2001
E30143		Vector for gene trapping and method for gene trapping by using said				
LOCUS		vector.				
DEFINITION		E30143				
ACCESSION		E30143				
VERSION		E30143.1	GI:13016987			
KEYWORDS		JP 1999332564-A/1.				
SOURCE		unidentified.				
ORGANISM		unclassified.				
REFERENCE		1 (bases 1 to 11206)				
AUTHORS		Rukachobitchi, T.A.2.Z. and Yamamoto, W.A.				
TITLE		Vector for gene trapping and method for gene trapping by using said				
JOURNAL		vector				
COMMENT		Patent: JP 1999332564-A 1 07-DEC-1999;				
		SCIENCE & TECH AGENCY				
		OS Unidentified				
		JP 1999332564-A/1				
		PN 07-DEC-1999				
		PF 22-MAY-1998				
		JP 1998141952				
		PI RUKACHOBITCHI TAMASSHU, ASUTAROSSHU ZORUDAN, DAISUKE YAMAMOTO,				







|||||  
Db 4081 ACTTTCTCGGAGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGCACTTCGCCCAAT 4140  
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Qy 4201 gtctggtccagccagcatgacgctgctcgtctcctcgagttcattcagggcaccggac 4260  
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DB	7381	AGTTTTTCAGAAAAATAATAATAATTTTCATTTTAACTCGCGAACATGTTGAAGATATGAATAT	7440
QY	7441	taatgaatcgagtaaacattttaatttcagatggttgcacatcttgattgacctcatct	7500
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QY	7441	TAATGAGATCGAGTAGACATTTAAATTTGCAGATGTTGCCATCTTGATTTGGCTTCATCT	7500
QY	7501	ttttgggccaaacaactcacgcaagtggcggtgatgaatatcaacgagggccatcttccctct	7560
DB	7501	TTTTTGGGCCAACACATCACGCAAGTGGCGGTGATGAATATCAACGAGGCCATCTTCTCTCT	7560
QY	7561	tccgtgacaaatgacatcttcaaaaacgtctttggccacgataaatgaagtcttgtaga	7620
DB	7561	TCCTTGACCAACATCACCTTTCAAAACGCTCTTTGCCACGATAAATGAAGTCTTGTTTAGA	7620
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AUTHORS	Lukacsovich, T., Asztalos, Z., Awano, W., Baba, K., Kondo, S., Niwa, S. and Yamamoto, D.		
TITLE	Dual-Tagging Gene Trap of Novel Genes in Drosophila melanogaster		
JOURNAL	Genetics 157 (2), 727-742 (2001)		
PUBMED	11156992		
REFERENCE	2 (bases 1 to 11207)		
AUTHORS	Lukacsovich, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-MAY-1999) Tamas Lukacsovich, Mitsubishi Kasei Inst. of Life Sci., ERATO, JST, Yamamoto Behavior Genes Project; 11 Minamiooya, Machida, Tokyo 194, Japan (E-mail: lukacs@fly.erato.jst.go.jp, Tel:81-427-212334, Fax:81-427-212850)		
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[illegible]



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Qy	10080	agcagaactttaaaagtgtctcatcatgttgaaaaagttcttcgggggcgaaaaactctcaagg	10139
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ACCESSION	U59056		
VERSION	U59056.1	GI:1432064	
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REFERENCE	P element transformation vector pCasper-hs		
AUTHORS	artificial sequence; vectors.		
TITLE	1 (bases 1 to 8780)		
JOURNAL	Thummel,C.S. and Pirrotta,V.		
REFERENCE	New pCasper P element vectors		
AUTHORS	Dros. Info. Service 71, 150-150 (1992)		
TITLE	2 (bases 1 to 8780)		
JOURNAL	Thummel,C.S. and Pirrotta,V.		
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source	Submitted (23-MAY-1996) Human Genetics, Univ. of Utah, Bldg. 533, Salt Lake City, UT 84112, USA		
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AUTHORS Thumel,C.S., Woodard,C.T. and Pirrotta,V.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-1996) Human Genetics, University of Utah, 5200
Eccles Institute, Bldg. 533, Salt Lake City, UT 84112, USA
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AUTHORS Pirrotta,V. and Zeng,C.  
JOURNAL Unpublished  
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AUTHORS Pirrotta,V.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1994) V. Pirrotta, Dept of Zoology, University of  
Geneva, 30 Quai E. Ansermet, 1211 Geneva, SWITZERLAND  
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Db 7794 AAAATTGCAATATTTCATTTTATTTTATTCACGTAAAGGTTAATGTTTCAAAAAA 7735  
QY 8336 attcgtccgcacacacaccttctctctcaacgaagcaacgtgcaactgaatttaagtgtata 8395  
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QY 8396 ctccggttaagctcggctatcacgagaccaccttatgtatttcatcatggtggccagacc 8455  
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Db 7674 CTTCCGTAAGCTTCGGCTATTCGACGGGACCACCTTATGTATTATTCATCATGGCCAGACC 7615  
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Db 4914 tttagccagatgcagcagcccggaagctcagatgagaatggccagac 4864

## RESULT 6

AF242362 10020 bp DNA circular SYN 16-JAN-2001  
LOCUS Green Pelican GFP transformation vector, complete sequence.  
DEFINITION AF242362  
ACCESSION AF242362  
VERSION AF242362.2 GI:12237296  
KEYWORDS  
SOURCE Green Pelican GFP transformation vector.  
ORGANISM Green Pelican GFP transformation vector  
artificial sequence; vectors.  
REFERENCE 1 (bases 1 to 10020)  
Barolo, S., Carver, L.A. and Posakony, J.W.  
GFP and beta-galactosidase transformation vectors for  
promoter/enhancer analysis in Drosophila  
Biotechniques 29 (4), 726-728 (2000)  
MEDLINE 20510562  
PUBMED 11056799  
REFERENCE 2 (bases 1 to 10020)  
Barolo, S.E. and Posakony, J.W.  
Direct Submission  
AUTHORS Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
JOURNAL  
REFERENCE 3 (bases 1 to 10020)  
Barolo, S.E. and Posakony, J.W.  
Direct Submission  
AUTHORS Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
JOURNAL  
REMARK Sequence update by submitter  
COMMENT On Jan 16, 2001 this sequence version replaced gi:9754906.  
FEATURES Location/Qualifiers  
1..10020  
/organism="Green Pelican GFP transformation vector"



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QY	6478	atgccacgacatctgaacctatcgccagcgagtgccgcgctggatcaggtgatccaggag	6537
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QY	6538	cttgcgtcagcaaatgctcagcacacgatacatcogtctgcccgcgaggtgaaaaagctctg	6597
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Db	3416	TTGGGCACCTCCAGGCAAGCCGTCGACTCTCTTTTCTAGTAGTTCGATGTGTTATTAA	3475
QY	6898	ggatatctagcattacattacatccaactccaactccacagcgtgggtgccagtgctctac	6957
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Db	3596	CGAGTCCCGTGTATCGGATCGCCAAAGATATGGGCACAATTTTGCTATTAGCAAGTAGCCCG	3655
QY	7078	ggatatgagcaggtgttggccaccacaaaatttggagaagccactggagcagccggagaa	7137
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Db	3716	TGGGTACACCTACAAGGCCACCTGGTGTATCGAGTTCGGCGCGTCTGTGGCGATGCTCG	3775
QY	7198	qctgtcgggtctcaaggaaccactcctcgtaaaagtcgacttattcagacacgcgtgag	7257
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AUTHORS	1. (bases 1 to 10095)		
TITLE	Barolo, S., Carver, L.A. and Posakony, J.W.		
JOURNAL	GFP and beta-galactosidase transformation vectors for		
MEDLINE	promoter/enhancer analysis in Drosophila		
PUBMED	Biotechniques 29 (4), 726-728 (2000)		
REFERENCE	2 (bases 1 to 10095)		
AUTHORS	Barolo, S.E. and Posakony, J.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall /		
	9500 Gilman Dr., La Jolla, CA 92093-0349, USA		
REFERENCE	3 (bases 1 to 10095)		
AUTHORS	Barolo, S.E. and Posakony, J.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall /		
	9500 Gilman Dr., La Jolla, CA 92093-0349, USA		
REMARK	Sequence update by submitter		
COMMENT	On Jan 16, 2001 this sequence version replaced gi:9754908.		
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AUTHORS	Barolo,S., Carver,L.A. and Posakony,J.W.		
TITLE	GFP and beta-galactosidase transformation vectors for promoter/enhancer analysis in Drosophila		
JOURNAL	BioTechniques 29 (4), 726-728 (2000)		
MEDLINE	20510582		
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REFERENCE	2 (bases 1 to 10288)		
AUTHORS	Barolo,S.E. and Posakony,J.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA		
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AUTHORS	Barolo,S.E. and Posakony,J.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA		
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AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.  
TITLE GFP and beta-galactosidase transformation vectors for  
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JOURNAL Biotechniques 29 (4), 726-728 (2000)  
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REFERENCE 2 (bases 1 to 13336)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
REFERENCE 3 (bases 1 to 13336)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
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AUTHORS Pirrotta,V.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1994) V. Pirrotta, Dept of zoology, University of  
Geneva, 30 Quai E. Ansermet, 1211 Geneva, SWITZERLAND  
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SOURCE	synthetic construct.
ORGANISM	synthetic construct
REFERENCE	artificial sequence.
AUTHORS	1 (bases 1 to 7775)
TITLE	Pirrotta,V.
JOURNAL	Direct Submission
COMMENT	Submitted (14-SEP-1994) V. Pirrotta, Dept of Zoology, University of Geneva, 30 Quai E. Ansermet, 1211 Geneva, SWITZERLAND
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JOURNAL Dros. Info. Service 71, 150-150 (1992)
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AUTHORS Thummel,C.S. and Pirrotta,V.
TITLE Direct Submission
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Db	4583	CCACAAATTTTCTTAAATAGCACACTTGGCAGCTGAATTAATTTTACTTCCAGTCACAG	4642
Qy	8304	-----	8303
Db	4643	CTTTGCAGCAAAATTTGCAATATTTTCATTTTTTTTTTATTTCCAGTAAGGTTAATGTTTT	4702
Qy	8327	caaaaaaatttcgtccgcacacacacttctctcctcaacagcaaaacgtgcactgaattt	8386
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Qy	8387	aagtataacttcggtaagcttcggctatcgacgggaccacacttatgttatttcatcgtg	8446
Db	4763	AAGTGTATACTTCGGTAAGCTTCGGCTATCGACGGGACCACTTATGTATTATTCATCATG	4822
Qy	8447	ggcacaacccactgaactcagcgcagatcgcgcgagagaagttaagcgtctccaggtat	8506
Db	4823	GGCCACCCACCTAGTCCAGCGCAGATCGCGCGGAGAGTTAAGCGTCTCCAGGAT	4882
Qy	8507	gaccttcgcgaactggcgacgtggttcgcagcagatgtgcagctaatctcccggtcc	8566
Db	4883	GACCTTCCCGAACTGGGCACGTGGTTCGACGATGTGCAGCTAATTTCCCGCGCTC	4942
Qy	8567	caqctccgcccatttggttaatacagcagacccctgttgcgtaacggaacatacgaggtta	8626
Db	4943	CAGCTCCGCCCAATTTGTTAATCAGCAGACCTCGTTTGGCGTAACGGAACCATGAGAGTA	5002
Qy	8627	cgaacaacatttgaggtatatactggcaccgagcccagattcaagaagaagcgtttttcca	8686
Db	5003	CGACACCAATTTGAGGTATCTAGGCACCCGAGCCCGAGTTCAAGAAGAGCGGTTTTTCCA	5062
Qy	8687	taggtccgcccccttgacgagcatcacaaaaatcgacgctcaagtcaaggtggcgaa	8746
Db	5063	TAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTTCAGAGTGGCGAAA	5122
Qy	8747	ccgcagagactataaagataccaggcgtttccccctgggaagctccctcgtcgtctccc	8806
Db	5123	CCGCAGAGACTATAAAGATACAGCGGTTTCCCGCTGGAAGTCCCTCGTCGCTCTCC	5182
Qy	8807	tgctccgacccctgcgcttacccgataaccttcgcgcttctcccttcgggaagcgtggc	8866
Db	5183	TGTTCCGACCTTCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGC	5242
Qy	8867	gctttcgaatgctcaacgctgtaggtatctcagtttcggttgtaggtcgttcgctccaagt	8926
Db	5243	GCTTTCTCAATGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTTCGCTCGCTCCAAGT	5302
Qy	8927	gggctgtgtgcagcaaccccccggttcagccgacgcgtcgccttatccggttaactatcg	8986
Db	5303	GGGCTGTGTGACAGAACCCCCGTTACGCCACCGCTGCGCTTATCCGCTTAATATCG	5362
Qy	8987	tcttgagtcacaacccggtaagacacgacttatcgcaactggcagcagcactggtaacag	9046
Db	5363	TCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTTGGCAGCAGCCTGTTAACAG	5422

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